

2.9e-116:590:95//U97670

R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence //2.2e-45:209:88//AC004050

R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64/L14331

R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128

R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038

R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces //1.4e-42:309:84//AC004882

R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence//6.4e-09:454:59//AC006024

R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154

R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172

R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626

R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622

R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984

R-PLACE1006782//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3,  
WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865

R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599

R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083

R-PLACE1006800//HS\_2270\_B1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence//4.1e-76:367:99//AQ085793

R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507

R-PLACE1006815//HS\_3028\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33;251:77//AQ120174

R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062

R-PLACE1006829

R-PLACE1006860

R-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378

R-PLACE1006878//Homo sapiens full-length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155

R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence//1.3e-38:283:85//AC004232

R-ռոտորոտորոտորոտ

R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62/Z82203

R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library)  
complete sequence//1.3e-42:305:87//AC005184

R-PLACE1006932

R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74/Z86061

R-nnnnnnnnnnnnn//Mouse mRNA for germ cell specific protein APG-1, complete cds.//9.5e-85:590:83//D49482

R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//6.7e-42:295.86//AC005544

R-PLACE1006962//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence //1 1e-19 302 71//AC002349

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4-PLACE1006989

R-PLACE1007014

R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845

R-PLACE1007045//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693

5 R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895

R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL021368

10 R-PLACE1007105//Mus musculus muskulin mRNA, complete cds.//2.7e-32:379:73//U72194

R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688

15 R-PLACE1007112//Cynops cornifex cytb gene.//0.020:427:58//AJ228479

R-PLACE1007132//Homo sapiens full-length insert cDNA YH77E09.//5.7e-107:535:96//AF074987

R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050

R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283

20 R-PLACE1007226

R-PLACE1007238

R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495

R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454

25 R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970

R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908

R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.4e-10:135:74//AC006080

30 R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291

R-PLACE1007282//B.garinii (strain TIs1) p83/100 gene (partial).//0.95:183:60//X81533

R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158

35 R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195

R-PLACE1007317//Drosophila dasyncemia 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253

40 R-PLACE1007342

R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870

R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507

45 R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709

R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261

R-PLACE1007402//HS\_2055\_A2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824

50 R-PLACE1007409//Homo sapiens mitoxanthrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771

R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594

R-PLACE1007450//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304

R-PLACE1007460

200408

R-PLACE1007460

R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-

brary) complete sequence//7.0e-08:335:60//AC004241

R-PLACE1007484

R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence//2.5e-05:421:61//AF072373

R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence//2.3e-09:577:57//AL034559

R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence//1.2e-79:387:96//AC004231

R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence//3.4e-09:148:73//AC003682

R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence//4.7e-38:297:82//AC004381

R-PLACE1007544

R-PLACE1007547//Human laminin alpha 4 chain (LAMA4\*-1) mRNA, complete cds//4.0e-17:108:97//U77706

R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence//2.2e-45:390:77//AC002465

R-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE//1.0e-56:302:95//AL031665

R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//1.5e-102:554:93//AF038179

R-PLACE1007618

R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//1.4e-103:537:94//AF038176

R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces//3.3e-76:289:94//AC005840

R-PLACE1007645//Homo sapiens full-length insert cDNA clone ZD76G10 //0.0080:96:77//AF086408

R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence//1.1e-82:412:97//AQ022149

R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence//0.0041:470:57//AE001367

R-PLACE1007688

R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence//1.3e-22:162:91//AC002044

R-PLACE1007697

R-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE//4.4e-121:624:95//AL031662

R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.8e-73:374:96//AF061243

R-PLACE1007725//Caenorhabditis elegans cosmid F38A5//0.070:186:60//U70854

R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR//3.8e-53:415:81//U60269

R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.1e-92:556:89//AB014585

R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence//4.0e-43:302:77//AF015169

R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence//1.0e-06:533:59//AL034560

R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds//0.28:386:58//M14820

R-PLACE1007791//D.discoideum gene for protein kinase//0.17:263:60//Z37981

R-PLACE1007807//Human DNA sequence from clone 878O8 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence//1.1e-72:324:88//AL031116

R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence//2.2e-14:325:67//AF017104

R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence//0.00052:455:61//AC002379

R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A)//0.0050:447:57//X95275

R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE//2.2e-111:570:95//AP000010

R-PLACE1007852//HS\_3028\_B2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey sequence//1.3e-12:209:71//AQ131021

R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//6.6e-110:574:94//AB018309

R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25.26.3. Contains a

R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence//1.6e-22

222.78//AC005754

brary) complete sequence//7.0e-08:335:60//AC004241

R-PLACE1007484

R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence//2.5e-05:421:61//AF072373

R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence//2.3e-09:577:57//AL034559

R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence//1.2e-79:387:96//AC004231

R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence//3.4e-09:148:73//AC003682

R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence//4.7e-38:297:82//AC004381

R-PLACE1007544

R-PLACE1007547//Human laminin alpha 4 chain (LAMA4\*-1) mRNA, complete cds//4.0e-17:108:97//U77706

R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence//2.2e-45:390:77//AC002465

R-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE//1.0e-56:302:95//AL031665

R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//1.5e-102:554:93//AF038179

R-PLACE1007618

R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//1.4e-103:537:94//AF038176

R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces//3.3e-76:289:94//AC005840

R-PLACE1007645//Homo sapiens full-length insert cDNA clone ZD76G10//0.0080:96:77//AF086408

R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence//1.1e-82:412:97//AQ022149

R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence//0.0041:470:57//AE001367

R-PLACE1007688

R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence//1.3e-22:162:91//AC002044

R-PLACE1007697

R-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE//4.4e-121:624:95//AL031662

R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.8e-73:374:96//AF061243

R-PLACE1007725//Caenorhabditis elegans cosmid F38A5//0.070:186:60//U70854

R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR//3.8e-53:415:81//U60269

R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.1e-92:556:89//AB014585

R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence//4.0e-43:302:77//AF015169

R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence//1.0e-06:533:59//AL034560

R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds//0.28:386:58//M14820

R-PLACE1007791//D.discoideum gene for protein kinase//0.17:263:60//Z37981

R-PLACE1007807//Human DNA sequence from clone 878O8 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence//1.1e-72:324:88//AL031116

R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence//2.2e-14:325:67//AF017104

R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence//0.00052:455:61//AC002379

R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A)//0.0050:447:57//X95275

R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE//2.2e-111:570:95//AP000010

R-PLACE1007852//HS\_3028\_B2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey sequence//1.3e-12:209:71//AQ131021

R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//6.6e-110:574:94//AB018309

R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25.26.3. Contains a

sequence//1.0e-43:412:97//AQ022149

R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34115 (LBNL H169), complete sequence//1.6e-22:222:78//AC005754

R-PLACE1007897//HS\_3113\_B2\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequencer.//2.9e-72:381:95//AQ186905

R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956

5 R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095

R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157

10 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530

R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529

R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262

15 R-PLACE1007990//E.tenella antigen LPMC61 mRNA, partial cds.//0.043:273:63//M30933

R-PLACE1008000//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346

R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628

20 R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840

R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592

R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232

25 R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036

R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157

30 R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.9e-11:384:63//AC005919

R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955

R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939

35 R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849

R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748

R-PLACE1008198

40 R-NNNNNNNNNNNN//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102

R-PLACE1008209//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549

R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688

R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562

45 R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-NNNNNNNNNNNN

R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272

R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308

50 R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886

R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176

R-PLACE100833//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226

R-NNNNNNNNNNNN

R-PLACE1008368//HS-1039-A1-C10-ME.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336

R-PLACE1007897//HS\_3113\_B2\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequencer.//2.9e-72:381:95//AQ186905

R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956

R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095

R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157

R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530

R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529

R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262

R-PLACE1007990//E.tenella antigen LPMC61 mRNA, partial cds.//0.043:273:63//M30933

R-PLACE1008000//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346

R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628

R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840

R-PLACE1008045//Homo sapiens chromosome 5. BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592

R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232

R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036

R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157

R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.9e-11:384:63//AC005919

R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955

R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939

R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849

R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748

R-PLACE1008198

R-PLACE1008209//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102

R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688

R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562

R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-PLACE1008280

R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272

R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308

R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886

R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176

R-PLACE1008333//Genomic sequence from Human 13 complete sequence.//1.0:176:65//AC001226

R-PLACE1008368

R-PLACE1008368//HS-1039-A1010-ME.abi.CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336

R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011

R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//1.0e-46:282:82//AC005244

5 R-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417

R-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604

R-nnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D86326

10 R-PLACE1008405//Human cosmidCRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//U15177

R-PLACE1008424

R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11 //7.5e-101:505:96//AB020864

15 R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576

R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335

R-PLACE1008455

20 R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526

R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696

R-PLACE1008488

25 R-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778

R-PLACE1008531//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555

R-PLACE1008532

30 R-PLACE1008533

R-PLACE1008568//HS\_3218\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623

R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074

35 R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.0e-78:498:86//AC006120

R-nnnnnnnnnnnn

R-PLACE1008626//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297

R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836

40 R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826

R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096

R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001

45 R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333

R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742

50 R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406

R-PLACE1008715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147

R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP.Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841

R-PLACE1008771

complete sequence.//0.99:111:51//AC005864

R-PLACE1008790//Hattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762

R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011

R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//1.0e-46:282:82//AC005244

R-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417

R-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604

R-nnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D86326

R-PLACE1008405//Human cosmidCRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//U15177

R-PLACE1008424

R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//7.5e-101:505:96//AB020864

R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576

R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335

R-PLACE1008455

R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526

R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696

R-PLACE1008488

R-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778

R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555

R-PLACE1008532

R-PLACE1008533

R-PLACE1008568//HS\_3218\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623

R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074

R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.0e-78:498:86//AC006120

R-nnnnnnnnnnnnn

R-PLACE1008626//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297

R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836

R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826

R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096

R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001

R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333

R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742

R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406

R-PLACE1008715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147

R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP.Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841

R-PLACE1008751

R-PLACE1008752

R-PLACE1008790//Rattus norvegicus clone 1 polymeric immunoglobulin receptor mRNA 3' untranslated region GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762



R-PLACE1008798//Homo sapiens full-length insert cDNA clone YZ86C05.//7.7e-58:285:100//AF086088  
 R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 2366014, genomic survey sequence.//3.5e-35:223:89//AQ079210  
 5 R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//AF030933  
 R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668  
 R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581  
 10 R-nnnnnnnnnnnnn/CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//8.9e-30:166:97//B93289  
 R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//AC005058  
 R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-37:585:67//AC004932  
 15 R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494\_G\_17, complete sequence.//0.0022:409:60//AC005820  
 R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308  
 R-PLACE1008925//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860  
 20 R-PLACE1008934  
 R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//9.8e-84:429:92//AC005495  
 R-PLACE1008947  
 R-PLACE1009020  
 25 R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117  
 R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391  
 R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//2.9e-06:160:70//AC004707  
 30 R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694  
 35 R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023  
 R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074  
 R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783  
 40 R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206  
 R-PLACE1009099  
 R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025  
 R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140  
 45 R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551  
 R-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929  
 R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031  
 50 R-PLACE1009158//Homo sapiens full-length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876  
 R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//2.8e-44:360:71//AC005972  
 R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046  
 55 R-PLACE1009174//Homo sapiens BAC clone 1009174, complete sequence.//1.1e-105:539:95//AF085876

R-PLACE1009175//Human DNA sequence from clone 1009175 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and

STSS, complete sequence.//1.9e-46:572:69//Z84480

R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070

R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560

R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248

R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//1.8e-75:364:85//AC005392

R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818

R-PLACE1009308

R-PLACE1009319//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801

R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//3.3e-87:576:85//AC006120

R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176

R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140

R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989

R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-Val.//1.1e-08:444:60//X05915

R-PLACE1009388

R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequencer.//0.065:279:61//AC002427

R-nnnnnnnnnnnn//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038

R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//9.8e-112:561:96//AC005919

R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120 R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598

R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151

R-PLACE1009459

R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531

R-PLACE1009477//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321

R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome-22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Armo, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160

R-PLACE1009539//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427

R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614

R-PLACE1009571//RPC111-61J16.TK RPC111 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146

R-PLACE1009581

R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006

R-PLACE1009596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051

R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230

R-PLACE1009612//Homo sapiens chromosome 11, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009613//Homo sapiens chromosome 11, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I7622z

R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey

STSS, complete sequence.//1.9e-46:572:69//Z84480

R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070

R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560

R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248

R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//1.8e-75:364:85//AC005392

R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818

R-PLACE1009308

R-PLACE1009319//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801

R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//3.3e-87:576:85//AC006120

R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176

R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140

R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989

R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-Val.//1.1e-08:444:60//X05915

R-PLACE1009388

R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequencer.//0.065:279:61//AC002427

R-nnnnnnnnnnnn//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038

R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//9.8e-112:561:96//AC005919

R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120 R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598

R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151

R-PLACE1009459

R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531

R-PLACE1009477//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321

R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome-22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Armo, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160

R-PLACE1009539//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427

R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614

R-PLACE1009571//RPCI11-61J16.TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146

R-PLACE1009581

R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006

R-PLACE1009596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051

R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230

R-PLACE1009613//Homo sapiens chromosome 11, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009614//Homo sapiens chromosome 11, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009621//Sequence 50 from patent US 5691147, 1.1e-06:20:235:73//U76222

R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey

sequence.//0.72:176:62//B81271

R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276

R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAI project).//0.013:521:58//AL021811

5 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159

R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534

R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011

R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109

10 R-PLACE1009731//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024

15 R-PLACE1009794

R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996

20 R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172

R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AG002672

25 R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945

R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-91:577:88//AC006116

R-nnnnnnnnnnnnn

30 R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005

R-PLACE1009924//HS\_3151\_B1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412

35 R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673

R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308

R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483

40 R-PLACE1009971//Homo sapiens full-length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247

R-PLACE1009992

R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367

45 R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874

R-PLACE1010023//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513

50 R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775

R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692

R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094

55 R-PLACE1010074//Homo sapiens chromosome 4, BAC clone F10M6 (ESSAI project), complete sequence.//0.013:521:58//AL021811

R-PLACE1010083

sequence.//0.72:176:62//B81271

R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B)//0.0068:396:59/X95276

R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)//0.013:521:58//AL021811

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159

R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534

R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence//2.8e-103:542:94//AC006011

R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence//4.6e-85:518:88//AC000109

R-PLACE1009731//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds //6.2e-116:598:95//AF046024

R-PLACE1009794

R-nnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence//7.5e-88:191:96//AL030996

R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69/Z98172

H-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence J/2.1e-29:230:76/AG002672

R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945

R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence//5.3e-91:577:88//AC006116

B-oooooooooooo

R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005

R-PLACE1009924//HS\_3151\_B1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412

R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey  
sequence//0.00010:159:68//B51673

R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308

R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483

R-PLACE1009971//Homo sapiens full-length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247

R-PLACE1009992

R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence//0.0019:305:61//AE001367

R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462,76//AC005874

R-PLACE1010023//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513

DOI: 10.1002/anie.201505516

R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to *C. elegans* Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775

R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein//1.9e-05:136:74//X84692

R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60;324:94//AQ042094

3. D. ACF 1010074 1140 40 01

4042 J. Inher. Metab. 17 (1994) 1039-1045

SS phase WORKING CHAR SEQUENCE, 4 unordered pieces //6.3e-08:489.58//AC005699

9 PLACE 1010083

R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59/B10583

R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411

R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556

R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374

R-PLACE1010106//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304

R-PLACE1010134

R-PLACE1010148//HS\_3128\_A1\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790

R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417

R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.6e-06:207:66//AC004928

R-PLACE101019411HS\_2232\_B1\_H10\_MR CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425

R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585

R-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AI 033377

R-PLACE1010261

R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, clone 85a6, reverse read cpg85a61rt1a.//0.068:171:63//Z63482

R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280

R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464

R-PLACE1010321

R-PLACE1010324//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149

R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024

R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.3e-31:418:66//AC004971

R-PLACE1010362

R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098

R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//1.4e-105:543:95//AC004675

R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137

R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

R-PLACE1010492//HS\_3169\_B2\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-nnnnnnnnnnnnn

R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929

R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein varl.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104 //0.00031:366:50//AF096370

R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-97:515:94//AC004846

R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59/B10583

R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411

R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556

R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374

R-PLACE1010106//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304

R-PLACE1010134

R-PLACE1010148//HS\_3128\_A1\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790

R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417

R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.6e-06:207:66//AC004928

R-PLACE101019411HS\_2232\_B1\_H10\_MR CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425

R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585

R-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377

R-PLACE1010261

R-PLACE1010270//H.sapiens CpG island DNA genomic Mse1 fragment, clone 85a6, reverse read cpg85a61rt1a.//0.068:171:63//Z63482

R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280

R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464

R-PLACE1010321

R-PLACE1010324//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149

R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024

R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.3e-31:418:66//AC004971

R-PLACE1010362

R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098

R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//1.4e-105:543:95//AC004675

R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137

R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

R-PLACE1010492//HS\_3169\_B2\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-nnnnnnnnnnnnn

R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929

R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein varl.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104 //0.00031:366:60//AF096370

5335

R-PLACE1010628//Homo sapiens clone DJ0647C14 WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-97:515:94//AC004846

R-PLACE1010629//HS\_3003\_A2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382

R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence.//9.4e-09:151:73//Z81467

R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300:95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400

R-PLACE1010743

R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//3.0e-103:511:97//AC005921

R-PLACE1010771

R-PLACE1010786

R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//1.8e-43:545:71//AC005682

R-PLACE1010802//Phoebe agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492:59//AF044862

R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524

R-PLACE1010833

R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153

R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11//4.9e-85:507:90//AB020868

R-PLACE1010870//RPC111-59K21:TK RPC111 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182

R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489

R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505

R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488

R-PLACE1010916//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557

R-PLACE1010917

R-PLACE1010925//HS\_2027\_B2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126

R-nnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441:93//AF064243

R-PLACE1010944

R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533

R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077

R-PLACE1010960//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21 WORKING DRAFT SEQUENCE

R-PLACE1010961//Homo sapiens clone 451B21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.041:444:84//Z95400

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome, segment 3/4.//0.59:345:61//

R-PLACE1010629//HS\_3003\_A2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382

R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence.//9.4e-09:151:73//Z81467

R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300:95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400

R-PLACE1010743

R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//3.0e-103:511:97//AC005921

R-PLACE1010771

R-PLACE1010786

R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//1.8e-43:545:71//AC005682

R-PLACE1010802//Phoebis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492:59//AF044862

R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524

R-PLACE1010833

R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153

R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11//4.9e-85:507:90//AB020868

R-PLACE1010870//RPC111-59K21:TK RPC111 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182

R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489

R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505

R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488

R-PLACE1010916//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557

R-PLACE1010917

R-PLACE1010925//HS\_2027\_B2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126

R-nnnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441:93//AF064243

R-PLACE1010944

R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533

R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077

R-PLACE1010960//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE

R-PLACE1010965//Homo sapiens clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome, segment 3/4.//0.59:345:61//

AJ235272

R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242

R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153

R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483

R-PLACE1011056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985

R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896

R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509

R-PLACE1011109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531

R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709

R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//44006

R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpg127a4.ft1a.//1.0:127:67//Z56550

R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333

R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968

R-PLACE1011185//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820

R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS\_3036\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587

R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659

R-PLACE1011229//HS\_3002\_B1\_E10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626

R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887

R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

R-PLACE1011472//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-PLACE1011473//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC 1171\_1\_10, complete sequence.//0.99:267:60//

AJ235272

R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242

R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153

R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483

R-PLACE1011056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985

R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896

R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509

R-PLACE1011109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531

R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14)//1.7e-29:179:94//Y16709

R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//44006

R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpg127a4.ft1a.//1.0:127:67//Z56550

R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333

R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968

R-PLACE1011185//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820

R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS\_3036\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587

R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659

R-PLACE1011229//HS\_3002\_B1\_E10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626

R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887

R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

R-PLACE1011472//Homo sapiens clone DJ0945F02

R-PLACE1011473//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-77:303:85//AC006013

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171\_L10, complete sequence.//0.99:267:60//

AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968

R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

R-PLACE1011567//Plasmodium-falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone. 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089

R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

R-PLACE1011783//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWDX312, complete sequence.//2.1e-100:511:95//AC004478

R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617

R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889

R-PLACE1011985

R-PLACE1011986

R-PLACE1011987//Human DNA sequence for RAB4013 protein, partial cds.//2.5e-104:540:95//AB018256

R-PLACE20000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000

AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968

R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

R-PLACE1011567//Plasmodium-falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone. 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089

R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

R-PLACE1011783//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.1e-100:511:95//AC004478

R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617

R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889

R-PLACE1011983

R-PLACE1011984

R-PLACE1011985//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256

R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524:95//AF091080  
 R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191  
 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//3.0e-55:299:86//  
 AC006236

R-PLACE2000021//CIT-HSP-2343C18. TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey sequence.//4.5e-54:295:94//AQ058140

R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298:82//X69907

R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-34:200:79//AC005628

R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274:89//AC003083

R-PLACE2000047//CIT-HSP-2373C2. TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey sequence.//1.8e-48:389:79//AQ112243

R-PLACE2000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING DRAFT SEQUENCE.//0.0027:95:76//AL022315

R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147

R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.9e-40:310:84//AC004832

R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219

R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910

R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285:84//AL031730

R-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559:97//AL031848

R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricel light chain, exon 1.//0.00041:347:61//X16325

R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067  
 R-PLACE2000132

R-PLACE2000136//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-30, complete sequence.//0.0032:310:61//AL008974

R-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//1.1e-111:566:96//AL020995

R-PLACE2000164

R-PLACE2000170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390:76//AC005598

R-PLACE2000172

R-PLACE2000176

R-PLACE2000187//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//8.7e-45:298:87//AL008718

R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495:92//L02897

R-PLACE2000223

R-PLACE2000235//HS\_3159\_B1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454:96//AQ179271

R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//9.1e-41:282:86//AC005902

R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181

R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:67//AC002394

R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//AC003043

R-PLACE2000305//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//AC003043

R-PLACE2000306//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//AC003043

R-PLACE2000311//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2. Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNC-

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524:95//AF091080  
 R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191  
 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//3.0e-55:299:86//  
 AC006236

R-PLACE2000021//CIT-HSP-2343C18. TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey se-  
 quence.//4.5e-54:295:94//AQ058140

R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298:82//X69907

R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-  
 34:200:79//AC005628

R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274:89//  
 AC003083

R-PLACE2000047//CIT-HSP-2373C2. TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey se-  
 quence.//1.8e-48:389:79//AQ112243

R-PLACE2000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1177I5, WORKING  
 DRAFT SEQUENCE.//0.0027:95:76//AL022315

R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147

R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//  
 5.9e-40:310:84//AC004832

R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219

R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SE-  
 QUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910

R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part  
 of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-  
 38:285:84//AL031730

R-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING  
 DRAFT SEQUENCE.//4.3e-113:559:97//AL031848

R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricel light chain, exon 1.//0.00041:347:61//  
 X16325

R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067  
 R-PLACE2000132

R-PLACE2000136//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-30, complete  
 sequence.//0.0032:310:61//AL008974

R-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING  
 DRAFT SEQUENCE.//1.1e-111:566:96//AL020995

R-PLACE2000164

R-PLACE2000170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390:76//AC005598

R-PLACE2000172

R-PLACE2000176

R-PLACE2000187//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING  
 DRAFT SEQUENCE.//8.7e-45:298:87//AL008718

R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495:92//L02897

R-PLACE2000223

R-PLACE2000235//HS\_3159\_B1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454:96//AQ179271

R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58  
 unordered pieces.//9.1e-41:282:86//AC005902

R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs  
 and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181

R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:  
 67//AC002394

R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//  
 AC003043

R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-  
 threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNC-

TION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence//4.0e-05:284:65//Z92542

R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.5e-26:334:70//AC006147

5 R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes//4.0e-05:254:64//AL021880

R-PLACE2000347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE//1.6e-82:504:88//AL022147

R-PLACE2000359//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 40E16, WORKING DRAFT SEQUENCE//2.0e-36:314:80//AL031963

10 R-PLACE2000366//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE//2.0e-48:389:80//AL031291

R-PLACE2000371

R-PLACE2000373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 324M8, WORKING DRAFT SEQUENCE//0.61:231:61//AL008734

15 R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence//3.5e-11:287:67//AC004917

R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence//6.8e-108:553:96//AL031432

R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces//2.9e-26:326:73//AC005059

20 R-PLACE2000399

R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence//6.5e-84:434:96//AC005216

H-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R)//0.47:104:70//Z54273

R-PLACE2000419

25 R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions//1.9e-40:447:74//AF003528

R-PLACE2000427

R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence//3.5e-40:286:85//AC000379

R-PLACE2000435

30 R-PLACE2000438//Homo sapiens full-length insert cDNA clone ZE04D01//2.2e-107:523:98//AF086521

R-PLACE2000450 4.1e-42:328:79//AG006257

R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete-sequence//5.1e-116:570:97//AC005740

35 R-PLACE2000465//Human BAC clone RG191D16, complete sequence//6.3e-37:408:75//AC002460

R-PLACE2000477//M.musculus tex264 mRNA (3'region)//7.5e-06:117:76//X80427

R-PLACE3000004

R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island//5.8e-34:308:78//Z82976

40 R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme//1.1e-36:273:87//Y17267

R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence//2.3e-10:181:71//AC004648

R-PLACE3000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE//1.2e-48:495:74//AL022156

45 R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence//3.4e-39:283:85//AC000026

R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence//9.2e-23:171:76//AC005200

R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23//0.00052:171:65//Y09645

50 R-PLACE3000142//HS\_3037\_82\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence//0.88:121:66//AQ097023

R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds//3.3e-23:472:66//AB001735

R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island//3.5e-11:176:73//Z49237

R-PLACE3000151

R-PLACE3000152

R-PLACE3000153//Homo sapiens DNA clone RG06/E16 from YAC 17d2 complete sequence//7.0e-38:545:70//AC002383

TION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence//4.0e-05:284:65//Z92542

R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.5e-26:334:70//AC006147

R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes//4.0e-05:254:64//AL021880

R-PLACE2000347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE//1.6e-82:504:88//AL022147

R-PLACE2000359//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 40E16, WORKING DRAFT SEQUENCE//2.0e-36:314:80//AL031963

R-PLACE2000366//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE//2.0e-48:389:80//AL031291

R-PLACE2000371

R-PLACE2000373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 324M8, WORKING DRAFT SEQUENCE//0.61:231:61//AL008734

R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence//3.5e-11:287:67//AC004917

R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence//6.8e-108:553:96//AL031432

R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces//2.9e-26:326:73//AC005059

R-PLACE2000399

R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence//6.5e-84:434:96//AC005216

R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R)//0.47:104:70//Z54273

R-PLACE2000419

R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions//1.9e-40:447:74//AF003528

R-PLACE2000427

R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence//3.5e-40:286:85//AC000379

R-PLACE2000435

R-PLACE2000438//Homo sapiens full-length insert cDNA clone ZE04D01//2.2e-107:523:98//AF086521

R-PLACE2000450 4.1e-42:328:79//AG006257

R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete-sequence//5.1e-116:570:97//AC005740

R-PLACE2000465//Human BAC clone RG191D16, complete sequence//6.3e-37:408:75//AC002460

R-PLACE2000477//M.musculus tex264 mRNA (3'region)//7.5e-06:117:76//X80427

R-PLACE3000004

R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island//5.8e-34:308:78//Z82976

R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme//1.1e-36:273:87//Y17267

R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence//2.3e-10:181:71//AC004648

R-PLACE3000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE//1.2e-48:495:74//AL022156

R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence//3.4e-39:283:85//AC000026

R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence//9.2e-23:171:76//AC005200

R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23//0.00052:171:65//Y09645

R-PLACE3000142//HS\_3037\_82\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence//0.88:121:66//AQ097023

R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds//3.3e-23:472:66//AB001735

R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island//3.5e-11:176:73//Z49237

R-PLACE3000155

R-PLACE3000155//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence//7.0e-38:545:70//AC002383

R-PLACE3000157

R-PLACE3000158//, complete sequence//1.4e-33:283:81//AC005500

R-PLACE3000160

R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence//5.2e-43:229:85//AC006130

R-PLACE3000194

R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence//7.2e-61:394:89//AC005291

R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene//0.23:309:57//U52112 R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence//1.1e-15:156:81//B54637

R-PLACE3000208//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING DRAFT SEQUENCE//1.3e-16:139:87//AL031594

R-PLACE3000218//HS\_3185\_B1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence//3.5e-07:120:75//AQ155720

R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence//2.4e-44:363:80//AC004167

R-PLACE3000226//Caenorhabditis elegans cosmid M01G5//0.88:95:77//AF078786

R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence//5.3e-69:536:81//U95626

R-PLACE3000242//Sequence 1 from patent US 5599918//3.2e-62:546:78//I35489

R-PLACE3000244//M.musculus mRNA for 200 kD protein//1.7e-45:404:75//X80169

R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//7.5e-28:174:94//AB002307

R-PLACE3000271//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE//3.9e-54:492:77//AL034379

R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence//5.4e-12:176:69//AC004081

R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence//5.7e-114:555:97//AC005328

R-PLACE3000310//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467L1, WORKING DRAFT SEQUENCE//6.2e-51:314:84//Z98884

R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds//2.5e-44:289:90//U93037

R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3//5.9e-20:153:88//M21006

R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.1e-43:230:84//AC005480

R-PLACE3000339

R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence//2.5e-111:550:97//AC006055

R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence//1.5e-44:314:78//AL022323

R-PLACE3000352//HS\_3095\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence//8.5e-73:356:99//AQ123142

R-PLACE3000353//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y22F5, WORKING DRAFT SEQUENCE//0.21:194:63//Z99712

R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7//0.26:360:60//AJ002197

R-PLACE3000363

R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence//4.6e-52:487:76//AC002465

R-PLACE3000373//HS\_3202\_B1\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence//2.4e-75:437:90//AQ252699

R-PLACE3000388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732F4, WORKING DRAFT SEQUENCE

R-PLACE3000399//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence//7.2e-61:394:89//AC005291

R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING

R-PLACE3000157

R-PLACE3000158//, complete sequence//1.4e-33:283:81//AC005500

R-PLACE3000160

R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence//5.2e-43:229:85//AC006130

R-PLACE3000194

R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence//7.2e-61:394:89//AC005291

R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene//0.23:309:57//U52112 R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence//1.1e-15:156:81//B54637

R-PLACE3000208//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING DRAFT SEQUENCE//1.3e-16:139:87//AL031594

R-PLACE3000218//HS\_3185\_B1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence//3.5e-07:120:75//AQ155720

R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence//2.4e-44:363:80//AC004167

R-PLACE3000226//Caenorhabditis elegans cosmid M01G5//0.88:95:77//AF078786

R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence//5.3e-69:536:81//U95626

R-PLACE3000242//Sequence 1 from patent US 5599918//3.2e-62:546:78//I35489

R-PLACE3000244//M.musculus mRNA for 200 kD protein//1.7e-45:404:75//X80169

R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//7.5e-28:174:94//AB002307

R-PLACE3000271//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE//3.9e-54:492:77//AL034379

R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence//5.4e-12:176:69//AC004081

R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence//5.7e-114:555:97//AC005328

R-PLACE3000310//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467L1, WORKING DRAFT SEQUENCE//6.2e-51:314:84//Z98884

R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds//2.5e-44:289:90//U93037

R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3//5.9e-20:153:88//M21006

R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.1e-43:230:84//AC005480

R-PLACE3000339

R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence//2.5e-111:550:97//AC006055

R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence//1.5e-44:314:78//AL022323

R-PLACE3000352//HS\_3095\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence//8.5e-73:356:99//AQ123142

R-PLACE3000353//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y22F5, WORKING DRAFT SEQUENCE//0.21:194:63//Z99712

R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7//0.26:360:60//AJ002197

R-PLACE3000363

R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence//4.6e-52:487:76//AC002465

R-PLACE3000373//HS\_3202\_B1\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence//2.4e-75:437:90//AQ252699

R-PLACE3000388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 730F1, WORKING DRAFT SEQUENCE//1.1e-43:230:84//AC005480

R-PLACE3000389//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence//5.2e-43:229:85//AC006130

R-PLACE3000399//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence//7.2e-61:394:89//AC005291

R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE

DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506

R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//8.0e-47:223:81//AC006023

R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003

R-PLACE3000405//Homo sapiens chromosome 7q telo BAC F6, complete sequence.//2.4e-44:466:74//AF104455

R-PLACE3000406//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718

R-PLACE3000413

R-PLACE3000416//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612

R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudogene, ESTs and STSs.//1.1e-41:366:78//AL008627

R-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43899

R-PLACE3000477

R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heyman nephritis antigen gp330.//6.6e-17:344:68//Z11995

R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352

R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984

R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//0.29:313:59//AC002379

R-PLACE4000052//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557

R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356

R-PLACE4000089//RPCI11-1511.TUB RPCI-11 Homo sapiens genomic clone RPCI-11-1511, genomic survey sequence.//3.2e-07:284:60//B82414

R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506

R-PLACE4000100

R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010

R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:90//AC003007

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969

R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034

R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939

R-PLACE4000192

R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631

R-PLACE4000233//Homo sapiens full-length insert cDNA YH59G06.//1.8e-79:414:97//AF074981

R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//5.7e-59:558:76//AC005821

R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381

R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.5e-39:311:83//AC005920

R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region.//0.33:197:61//Z80410

R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:337:77//U43899

R-PLACE4000270//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939

R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339

R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete

DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506

R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//8.0e-47:223:81//AC006023

R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003

R-PLACE3000405//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//2.4e-44:466:74//AF104455

R-PLACE3000406//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718

R-PLACE3000413

R-PLACE3000416//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612

R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudogene, ESTs and STSs.//1.1e-41:366:78//AL008627

R-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43899

R-PLACE3000477

R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heyman nephritis antigen gp330.//6.6e-17:344:68//Z11995

R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352

R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984

R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//0.29:313:59//AC002379

R-PLACE4000052//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557

R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356

R-PLACE4000089//RPCI11-1511.TUB RPCI-11 Homo sapiens genomic clone RPCI-11-1511, genomic survey sequence.//3.2e-07:284:60//B82414

R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506

R-PLACE4000100

R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010

R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:90//AC003007

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969

R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034

R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939

R-PLACE4000192

R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631

R-PLACE4000233//Homo sapiens full-length insert cDNA YH59G06.//1.8e-79:414:97//AF074981

R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//5.7e-59:558:76//AC005821

R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381

R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.5e-39:311:83//AC005920

R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region.//0.33:197:61//Z80410

R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25 complete sequence.//1.4e-31:327:76//AF034441

R-PLACE4000271//Homo sapiens clone YH59G06, derived precursor protein, complete cds.//1.4e-79:414:97//AF074981

R-PLACE4000339//Sequence B from patent US 5744300.//0.0017:51:98//AR003339

R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete

sequence//8.2e-41:295:85//Z99495

R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence//1.3e-32:404:75//U73640

R-PLACE4000326

R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence//0.32:135:68//AC005587

R-PLACE4000367//H.sapiens gene encoding RING finger protein//0.61:146:67//Y07829

R-PLACE4000369//HS\_3181\_A1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence//7.1e-80:424:94//AQ173222

R-PLACE4000379//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE//1.7e-05:160:65//AL022312

R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces//2.4e-47:351:81//AC004913

R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence//8.5e-88:541:88//AL034377

R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces//2.7e-17:143:83//AC000406

R-PLACE4000411

R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces//0.028:91:78//AC005628

R-PLACE4000465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE//1.6e-43:532:71//AL022156

R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence//4.1e-06:357:61//AE001427

R-PLACE4000494//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence//2.7e-37:416:74//AC005865

R-PLACE4000522

R-PLACE4000548//Homo sapiens 12p13.3 PAC RPC15-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence//0.0020:383:60//AC005342

R-PLACE4000558//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC Library) complete sequence//2.9e-44:465:75//AC002996

R-THYRO1000026//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING DRAFT SEQUENCE//2.2e-43:354:82//Z83844

R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence//0.022:327:60//AE001422

R-THYRO1000035//HS\_3018\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence//2.3e-36:228:91//AQ092318

R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces//1.0:367:56//AC004157

R-THYRO1000070//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.1/1e-44:284:89//U14573

R-THYRO1000072//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence//6.6e-33:150:83//U14567

R-THYRO1000085

R-THYRO1000092//Homo sapiens chromosome 7qtelo BAC F6, complete sequence//3.3e-36:301:78//AF104455

R-THYRO1000107//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE//1.4e-35:282:82//AL033528

R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence//4.0e-32:351:65//AC002300

R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence//6.6e-77:507:85//U91318

R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces//0.66:334:59//AC005840

R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//2.3e-88:449:96//AF087142

R-THYRO1000132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE//1.1e-40:298:84//Z95114

R-THYRO1000156//Homo sapiens chromosome 17, clone hRPK 849 N 15, complete sequence//2.4e-37:105:73//AC005703

R-THYRO1000169//Homo sapiens genomic clone 443, complete sequence//8.4e-08:276:84//B03536

R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island//1.1e-

sequence.//8.2e-41:295:85//Z99495

R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640

R-PLACE4000326

R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//AC005587

R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829

R-PLACE4000369//HS\_3181\_A1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222

R-PLACE4000379//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312

R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913

R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377

R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC000406

R-PLACE4000411

R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.028:91:78//AC005628

R-PLACE4000465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-43:532:71//AL022156

R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:357:61//AE001427

R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-37:416:74//AC005865

R-PLACE4000522

R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.0020:383:60//AC005342

R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.9e-44:465:75//AC002996

R-THYRO1000026//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING DRAFT SEQUENCE.//2.2e-43:354:82//Z83844

R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:327:60//AE001422

R-THYRO1000035//HS\_3018\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318

R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157

R-THYRO1000070//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.1/1e-44:284:89//U14573

R-THYRO1000072//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567

R-THYRO1000085

R-THYRO1000092//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//3.3e-36:301:78//AF104455

R-THYRO1000107//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528

R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-32:351:65//AC002300

R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:85//U91318

R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.66:334:59//AC005840

R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142

R-THYRO1000132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//1.1e-40:298:84//Z95114

R-THYRO1000156//Homo sapiens chromosome 17 clone hRPK 849 N 15, complete sequence.//2.4e-37:150:83//U14567

R-THYRO1000163//Homo sapiens chromosome 17 clone hRPK 849 N 15, complete sequence.//2.4e-37:150:83//U14567

R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-

70:553:81//Z83841

R-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 41018, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732

R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43:356:80//U18271

R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//2.6e-40:386:77//AC004139

R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.1e-108:535:97//AJ005698

R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.4e-113:559:97//AB014552

R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:318:86//D84482

R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115

R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//4.8e-58:447:81//AC000039

R-THYRO 1000242

R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//3.4e-56:300:84//Z95152

R-THYRO1000270

R-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664

R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068

R-THYRO1000320//HS\_2033\_B1\_A07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence.//0.97:211:63//AQ233366

R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058

R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333

R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//4.6e-47:317:87//U29091

R-THYRO1000368//HS\_3049\_A1\_E12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey sequence.//7.0e-11:111:83//AQ126777

R-nnnnnnnnnnnnn

R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//2.4e-101:545:93//AC006019

R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078

R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523

R-THYRO 1000401

3.3e-111:546:97//AF051907

R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.7e-44:289:89//AC005231

R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//6.7e-27:222:82//AC005668

R-THYRO1000471//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391

R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962

R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740

R-THYRO1000501//HS\_2208\_A1\_G11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586

R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987

R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798

R-THYRO1000558

R-THYRO 1000569

R-THYRO1000570

R-THYRO1000571//Homo sapiens protein associated with Myc mRNA, complete cds.//1.1e-99:97:45//AF005596

R-THYRO1000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072

70:553:81//Z83841

R-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 41018, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732

R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43:356:80//U18271

R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//2.6e-40:386:77//AC004139

R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.1e-108:535:97//AJ005698

R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.4e-113:559:97//AB014552

R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:318:86//D84482

R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115

R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//4.8e-58:447:81//AC000039

R-THYRO 1000242

R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//3.4e-56:300:84//Z95152

R-THYRO1000270

R-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664

R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068

R-THYRO1000320//HS\_2033\_B1\_A07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence.//0.97:211:63//AQ233366

R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058

R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333

R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//4.6e-47:317:87//U29091

R-THYRO1000368//HS\_3049\_A1\_E12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey sequence.//7.0e-11:111:83//AQ126777

R-nnnnnnnnnnnnn

R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//2.4e-101:545:93//AC006019

R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078

R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523

R-THYRO 1000401

3.3e-111:546:97//AF051907

R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.7e-44:289:89//AC005231

R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//6.7e-27:222:82//AC005668

R-THYRO1000471//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391

R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962

R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740

R-THYRO1000501//HS\_2208\_A1\_G11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586

R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987

R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798

R-THYRO1000558

R-THYRO 1000569

R-THYRO 1000570

R-THYRO 1000596//Mus musculus c-myc associated with Myc mRNA, complete cds.//8.1e-117:533:97//AF005966

R-THYRO 1000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072

R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675  
R-THYRO 1000605  
R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//  
AC005546  
5 R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs  
and GSSs, complete sequence.//4.0e-06:249:63//AL022323  
R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998  
R-THYRO1000658//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572  
R-nnnnnnnnnnnnn  
10 R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains  
endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005  
R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:  
64//AC004069  
R-THYRO1000684  
15 R-THYRO1000699  
R-THYRO1000712  
R-THYRO1000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:468:64//AC002460  
R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533  
R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660  
20 R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558  
R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey se-  
quence.//1.2e-81:391:99//AQ036226  
R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//9.4e-07:494:58//  
AC004617  
25 R-THYRO1000793  
R-THYRO1000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
DRAFT SEQUENCE.//1.7e-42:379:79//Z93014  
R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered piec-  
es.//4.7e-40:362:76//AC002555  
30 R-THYRO1000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
DRAFT SEQUENCE.//4.0e-58:295:92//Z82199  
R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788  
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angel-  
man Syndrome region, complete sequence.//3.3e-57:522:76//AC004738  
35 R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE,  
9 unordered pieces.//4.2e-17:291:69//AC005849  
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs,  
complete sequence.//1.1e-41:419:75//AL031592  
R-THYRO1000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORK-  
40 ING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549  
R-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING  
DRAFT SEQUENCE.//3.7e-111:569:96//AL031719  
R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
1.0e-97:554:92//AC006015  
45 R-THYRO1000926//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:  
566:94//AF079529  
R-THYRO1000934//Homo sapiens full-length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378  
R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 un-  
ordered pieces.//8.9e-61:479:81//AC004229  
50 R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639  
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//  
AF047440  
R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//  
AC006126

AC005556

R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ698p12 containing uteroglobin gene  
WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078

R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675  
R-THYRO 1000605  
R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//  
AC005546  
5 R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs  
and GSSs, complete sequence.//4.0e-06:249:63//AL022323  
R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998  
R-THYRO1000658//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572  
R-nnnnnnnnnnnnn  
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endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005  
R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:  
64//AC004069  
R-THYRO1000684  
15 R-THYRO1000699  
R-THYRO1000712  
R-THYRO1000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:468:64//AC002460  
R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533  
R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660  
20 R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558  
R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey se-  
quence.//1.2e-81:391:99//AQ038226  
R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//9.4e-07:494:58//  
AC004617  
25 R-THYRO1000793  
R-THYRO1000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING  
DRAFT SEQUENCE.//1.7e-42:379:79//Z93014  
R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered piec-  
es.//4.7e-40:362:76//AC002555  
30 R-THYRO1000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING  
DRAFT SEQUENCE.//4.0e-58:295:92//Z82199  
R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788  
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angel-  
man Syndrome region, complete sequence.//3.3e-57:522:76//AC004738  
35 R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE,  
9 unordered pieces.//4.2e-17:291:69//AC005849  
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs,  
complete sequence.//1.1e-41:419:75//AL031592  
R-THYRO1000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORK-  
40 ING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549  
R-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING  
DRAFT SEQUENCE.//3.7e-111:569:96//AL031719  
R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
1.0e-97:554:92//AC006015  
45 R-THYRO1000926//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:  
566:94//AF079529  
R-THYRO1000934//Homo sapiens full-length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378  
R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 un-  
ordered pieces.//8.9e-61:479:81//AC004229  
50 R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639  
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//  
AF047440  
R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//  
AC006126

00556.

R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene,  
WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence//6.7e-39:292:78//Z84466

R-THYRO1001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence//2.5e-39:310:83//AQ253727

R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence//2.5e-50:300:88//Z84466

R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence//5.1e-26:143:100//B56677

R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence//1.4e-48:316:87//AQ239882

R-THYRO1001093

R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence//0.47:102:73//AC005070

R-THYRO1001120

R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//8.9e-81:429:94//AJ006417

R-THYRO1001133//CIT-HSP-2381110.TR CIT-HSP Homo sapiens genomic clone 2381110, genomic survey sequence//4.7e-12:237:67//AQ111077

R-THYRO1001134

R-THYRO1001142//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81d1, reverse read cpg81d1.rt1a.//0.95:214:60//Z56037

R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence//4.6e-26:262:77//B04145

R-THYRO1001177

R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//1.0e-41:281:87//AC003973

R-THYRO 1001204

R-THYRO1001213//Human Alu repeat sequence A6//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK.16\_A\_1, complete sequence//8.7e-53:442:79//AC006227

R-THYRO1001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces//0.53:330:61//AC004630

R-THYRO 1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic Mse1 fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783

R-THYRO1001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE//3.0e-58:476:80//Z82207

R-THYRO100132//Plasmodium falciparum MAL3P2, complete sequence//1.0e-08:408:62//AL034558

R-nnnnnnnnnnnnn

R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds//3.2e-08:266:64//AB018288

R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence//1.8e-109:584:94//AC005660

R-THYRO1001374

R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds//4.2e-51:333:88//U29953

R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPC11-69F22.TK RPC11 Homo sapiens genomic clone R-69F22, genomic survey sequence//1.9e-67:400:90//AQ238297

R-THYRO1001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE//2.2e-06:349:63//AL031123

R-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE//2.2e-89:506:86//AJ002553

R-THYRO1001434//Microcentus caryae 12S mitochondrial cytochrome b DNA, complete cds

R-THYRO1001458//Human

R-THYRO1001458//Human DNA sequence from clone 458, chromosome 10q24.1, complete sequence//3.3e-07:196:67//AL021578 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence//3.3e-07:196:67//AL021578

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466

R-THYRO1001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727

R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466

R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677

R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882

R-THYRO1001093

R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070

R-THYRO1001120

R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//8.9e-81:429:94//AJ006417

R-THYRO1001133//CIT-HSP-2381110.TR CIT-HSP Homo sapiens genomic clone 2381110, genomic survey sequence.//4.7e-12:237:67//AQ111077

R-THYRO1001134

R-THYRO1001142//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81d1, reverse read cpg81d1.rt1a.//0.95:214:60//Z56037

R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145

R-THYRO1001177

R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973

R-THYRO 1001204

R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK.16\_A\_1, complete sequence.//8.7e-53:442:79//AC006227

R-THYRO1001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630

R-THYRO 1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic Mse1 fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783

R-THYRO1001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207

R-THYRO100132//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558

R-nnnnnnnnnnnnn

R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288

R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660

R-THYRO1001374

R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953

R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPC11-69F22.TK RPC11 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297

R-THYRO1001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123

R-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553

R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, complete sequence.//1.0e-08:408:62//AL034558

R-THYRO1001458//Human DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466

R-THYRO1001458//Human DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466  
syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP L MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578

R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered piece//1.2e-99:517:95//AC006001

R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces//8.5e-14:221:70//AC004085

R-THYRO10001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence//0.00012:141:68//AQ182326

R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence//0.42:323:60//AL023876

R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//1.7e-42:370:78//AC005077

R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.0:144:67//AC005868

R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.43:268:61//AC005308

R-THYRO1001573//M.avium rpsL gene//0.98:131:66//X80120

R-THYRO1001584//A.longa plastid genes for ribosomal proteins and tRNAs//0.29:502:58//X75653

R-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE//1.5e-33:319:78//AL023808

R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence//4.4e-13:320:67//AC005919

R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X//1.9e-32:391:76//Z77249

R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT)//1.9e-61:448:92//AJ002190

R-THYRO1001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING DRAFT SEQUENCE//5.4e-41:381:78//AL031671

R-THYRO1001656//HS\_2201\_B2\_A08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence//0.096:162:63//AQ293168

R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds//1.0:229:62//U22954

R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//4.8e-110:562:95//AJ225089

R-THYRO1001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence//1.5e-17:224:68//AQ042426

R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence//1.6e-44:251:93//AF091072

R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence//1.8e-26:378:68//AC006011

R-THYRO1001721//, complete sequence//1.3e-101:571:92//AC005500

R-nnnnnnnnnnnnn

R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence//1.1e-15:193:70//AC004777

R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3//0.54:260:61//M88244

R-THYRO1001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE//1.6e-12:285:64//AL022156

R-THYRO1001793

R-THYRO1001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE//2.5e-43:486:74//AL031728

R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence//5.0e-41:245:87//AC005696

R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence//4.4e-12:419:61//AC005137

R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS11109 from Zet14-15, complete sequence//0.9:112:57:97

R-Y79AA1000037//Homo sapiens BAC clone GS11109 from Zet14-15, complete sequence//0.9:112:57:97  
R-Y79AA1000037//Homo sapiens BAC clone GS11109 from Zet14-15, complete sequence//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence//6.1e-

R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered piece//1.2e-99:517:95//AC006001

R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces//8.5e-14:221:70//AC004085

R-THYRO10001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence//0.00012:141:68//AQ182326

R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence//0.42:323:60//AL023876

R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//1.7e-42:370:78//AC005077

R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.0:144:67//AC005868

R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.43:268:61//AC005308

R-THYRO1001573//M.avium rpsL gene//0.98:131:66//X80120

R-THYRO1001584//A.longa plastid genes for ribosomal proteins and tRNAs//0.29:502:58//X75653

R-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE//1.5e-33:319:78//AL023808

R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence//4.4e-13:320:67//AC005919

R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X//1.9e-32:391:76//Z77249

R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT)//1.9e-81:448:92//AJ002190

R-THYRO1001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING DRAFT SEQUENCE//5.4e-41:381:78//AL031671

R-THYRO1001656//HS\_2201\_B2\_A08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence//0.096:162:63//AQ293168

R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds//1.0:229:62//U22954

R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//4.8e-110:562:95//AJ225089

R-THYRO1001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence//1.5e-17:224:68//AQ042426

R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence//1.6e-44:251:93//AF091072

R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence//1.8e-26:378:68//AC006011

R-THYRO1001721//, complete sequence//1.3e-101:571:92//AC005500

R-nnnnnnnnnnnnn

R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence//1.1e-15:193:70//AC004777

R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3//0.54:260:61//M88244

R-THYRO1001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE//1.6e-12:285:64//AL022156

R-THYRO1001793

R-THYRO1001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE//2.5e-43:486:74//AL031728

R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence//5.0e-41:245:87//AC005696

R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence//4.4e-12:419:61//AC005137

R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14 p15, complete sequence//2.9e-112:551:67

R-Y79AA1000037//Homo sapiens BAC clone GS114I09 from 7p14 p15, complete sequence//2.9e-112:551:67

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence//6.1e-

56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5//0.64:203:63//D21079

R-Y79AA1000131//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cyttauxzoon felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=O, genomic survey sequence.//6.4e-52:348:88//AQ090225

R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047

R-Y79AA10003131//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540

R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692

R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey sequence.//0.10:171:65//B88000

R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037

R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-86:221:90//AC005033

R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282

R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59//AC006143

R-Y79AA1000540//Z.diploperemnis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325

R-Y79AA1000627//Homo sapiens full-length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117

R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.//4.6e-88:429:98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PEYAC181 gene for PEXAC181, complete cds.//0.00013:52:100//D78611

R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3'region).//1.1e-06:104:78//X80427

56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5//0.64:203:63//D21079

R-Y79AA1000131//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

5 R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

10 R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cyttauxoon felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=O, genomic survey sequence.//6.4e-52:348:88//AQ090225

15 R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047

R-Y79AA10003131//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540

20 R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692

25 R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey sequence.//0.10:171:65//B88000

30 R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037

R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-86:221:90//AC005033

35 R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282

40 R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59//AC006143

R-Y79AA1000540//Z.diploperemnis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325

R-Y79AA1000627//Homo sapiens full-length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117

45 R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.//4.6e-88:429:98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

50 R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12, PEXAC186 gene, complete cds.//0.00013:52:100//D78611

R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//0.015:322:60//Z93851

R-Y79AA1000800//M.musculus tex264 mRNA (3'region).//1.1e-06:104:78//X80427

R-nnnnnnnnnnnn//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642

R-Y79AA1000824//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey sequence.//3.3e-60:295:100//AQ061422

R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823

R-Y79AA1001023

R-Y79AA1001041

R-Y79AA1001048

R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//1.2e-60:537:78//AC004626

R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.3e-41:405:77//AC005031

R-Y79AA1001077

R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801

R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639//0.0072:309:63//U40259

R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068

R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012

R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048

R-Y79AA1001185

R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC005912

R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112

R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355

R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594

R-Y79AA1001391//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:63//AC004221

R-Y79AA1001493

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs.

R-nnnnnnnnnnnn/CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642

R-Y79AA1000824//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey sequence.//3.3e-60:295:100//AQ061422

R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823

R-Y79AA1001023

R-Y79AA1001041

R-Y79AA1001048

R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//1.2e-60:537:78//AC004626

R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.3e-41:405:77//AC005031

R-Y79AA1001077

R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801

R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639//0.0072:309:63//U40259

R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068

R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012

R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048

R-Y79AA1001185

R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC005912

R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112

R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355

R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594

R-Y79AA1001391//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:63//AC004221

R-Y79AA1001402//Homo sapiens Chromosome 11 BAC clone R29144

R-Y79AA1001403//Homo sapiens Chromosome 11 BAC clone R29144

R-Y79AA1001404

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs.

complete sequence.//1.3e-35:207:95//AL034430

R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336

R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574

R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151

R-Y79AA1001555

R-Y79AA1001585

R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722

R-Y79AA1001603//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766

R-Y79AA1001613

R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975

R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008

R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743

R-nnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792

R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178

R-Y79AA1001705

R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ho gene, partial cds.//2.2e-45:554:75//AF042139

R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402

R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044

R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:557:89//U74297

R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152

R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369

R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0089:527:58//AB016874

R-Y79AA1001874

R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577

R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377:81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612

R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 2328I21, genomic survey sequence.//1.9e-44:245:96//AQ044502

R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752

R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15J6, genomic survey sequence.//8.5e-21:147:91//B75354

R-Y79AA1002139

R-Y79AA1002204

R-Y79AA1002209//Homo sapiens genomic clone 2209, genomic survey sequence.//1.0:138:68//AL022577

R-Y79AA1002210

complete sequence//1.3e-35:207:95//AL034430

R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds //2.7e-44:285:81/D14336

R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence //0.70:365:60//AL023574

R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151

R-Y79AA1001555

R-Y79AA1001585

R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722

R-Y79AA1001603//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72f8, forward read cpG72f8.ft1a.//3.3e-21:131:96//Z62766

R-Y79AA1001613

R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975

R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15,  
WORKING DRAFT SEQUENCE.//3.2e-11:114:84/AP000008

R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743

R-nnnnnnnnnnnn/RPCL11-42M5.TJ RPCL11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//  
0.013:64:89//AQ052792

R-Y79AA1001696//*Apis mellifera ligustica* complete mitochondrial genome//9.3e-09:428:58//L06178

R-Y79AA1001705

R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds./2.2e-45:554:75//AF042139

R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence//1.0:414:57//AE001402

R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING  
DRAFT SEQUENCE.//2.8e-05:329:61//Z98044

R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:557:89/U74297

R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152

R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//114369

R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//  
0.0089:527:58//AB016874

R-Y79AA1001874

R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence//1.0:138:68//AL022577

R-Y79AA1002027//Liverwort *Marchantia polymorpha* chloroplast genome DNA.//0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence \*\* SEQUENCING IN PROGRESS \*\*\* from clone 172B20, WORKING  
DRAFT SEQUENCE //1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377.81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612

R-Y79AA1002103//CIT-HSP-2328121.TR CIT-HSP Homo sapiens genomic clone 2328121, genomic survey sequence.//1.9e-44;245:96//AQ044502

R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752

R-Y79AA1002125//RPC11-15J6.TV RPC1-11 Homo sapiens genomic clone RPC1-11-15J6, genomic survey sequence.//8.5e-21:147.91//B75354

R-Y79AA1002139

• **Adaptation:** The process by which an organism's traits change over time to better suit its environment.

[illegible]

UAA1002209.1: deduced aa. 11 gene for reverse transcriptase (P:4) 100.106.65//X6541b

0-Y79AA1002210

R-Y79AA1002211//H.sapiens NGAL gene//1.0:311:59//X99133  
 R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 DRAFT SEQUENCE.//5.9e-07:535:57//AL034557

R-Y79AA1002229

5 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592

R-Y79AA1002246

R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds//1.3e-92:453:97//AB013384

R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331

10 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534

R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173112 map 10q25, complete sequence.//  
 1.1e-07:368:61//AC005887

R-Y79AA1002351

15 R-Y79AA1002361//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65b9, reverse read cpg65b9.rt1a.//  
 0.57:59:79//Z62206

R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//2.0e-98:385:99//  
 AC005920

R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//5.4e-59:490:  
 76//AC004662

20 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
 quence.//6.3e-08:103:80//AC004087

R-Y79AA1002431

R-nnnnnnnnnnnr//Mouse transcriptional control element.//0.064:84:71//M17284

25 R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence.//1.6e-  
 103:525:96//AC006116

R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//9.7e-38:302:  
 83//AC006238

R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

30 Homology Search Result Data 4.

[0307] The result of the homology search of the Human Unigene using the clone sequence of 5'-end.

[0308] Data include

35 the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

40 [0309] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069

F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:  
 L40157

45 F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668

F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078

F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247

F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharo-  
 myces cerevisiae]//0.00019:192:65//Hs.7900:W22411

50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759

F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910

F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734

F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:  
 342:61//Hs.14207:U86453

F-HEMBA1000130

F-HEMBA1000134

F-HEMBA1000135//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200

F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

R-Y79AA1002211//H.sapiens NGAL gene//1.0:311:59//X99133  
 R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
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 5 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592  
 R-Y79AA1002246  
 R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:97//AB013384  
 R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331  
 10 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534  
 R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173112 map 10q25, complete sequence.//  
 1.1e-07:368:61//AC005887  
 R-Y79AA1002351  
 R-Y79AA1002361//H.sapiens CpG island DNA genomic MseI fragment, clone 65b9, reverse read cpg65b9.rt1a.//  
 15 0.57:59:79//Z62206  
 R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//2.0e-98:385:99//  
 AC005920  
 R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//5.4e-59:490:  
 76//AC004662  
 20 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
 quence.//6.3e-08:103:80//AC004087  
 R-Y79AA1002431  
 R-nnnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17284  
 R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence.//1.6e-  
 25 103:525:96//AC006116  
 R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//9.7e-38:302:  
 83//AC006238  
 R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

# 30 Homology Search Result Data 4.

[0307] The result of the homology search of the Human Unigene using the clone sequence of 5'-end.

[0308] Data include

35 the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

40 [0309] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069  
 F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:  
 L40157  
 45 F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668  
 F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078  
 F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247  
 F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharo-  
 myces cerevisiae]//0.00019:192:65//Hs.7900:W22411  
 50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759  
 F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910  
 F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734  
 F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:  
 342:61//Hs.14207:U86453  
 F-HEMBA1000130//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200  
 F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

Hs.135552:AI215187

F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309

F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079

5 F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [H.sapiens]//1.3e-18:111:96//Hs.163863:W28729

F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802

F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133

F-HEMBA1000201//Human Ini1 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847

10 F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529

F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984

F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289

F-HEMBA1000231

15 F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377

F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703

F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460

F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562

F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568

20 F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186

F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406

F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664

F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI206095

F-HEMBA1000303

25 F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946

F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898

F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965

F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961

30 F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712

F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503

F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548

F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802

F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087

35 F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010

F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853

F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878

F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520

40 F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533

F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008

F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915

F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253

F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875

45 F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.159897:AB007970

F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034

F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398

F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893

50 F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875

F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590

F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853

F-HEMBA1000469

F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//1.9e-58:441:78//Hs.154326:D42087

F-HEMBA1000490//Homo sapiens kinesin mRNA, complete cds//1.5e-48:266:95//Hs.160642:AI240133

F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970

F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750

Hs.135552:AI215187

F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309

F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079

5 F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [H.sapiens]//1.3e-18:111:96//Hs.163863:W28729

F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802

F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133

F-HEMBA1000201//Human Ini1 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847

10 F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529

F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984

F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289

F-HEMBA1000231

15 F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377

F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703

F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460

F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562

F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568

20 F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186

F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406

F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664

F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI206095

F-HEMBA1000303

25 F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946

F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898

F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965

F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961

30 F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712

F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503

F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548

F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802

F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087

35 F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010

F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853

F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878

F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520

40 F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533

F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008

F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915

F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253

F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875

45 F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.159897:AB007970

F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034

F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398

F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893

50 F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875

F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590

F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853

F-HEMBA1000469

F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (ERT1) mRNA, complete cds//1.5e-053:58:44:104:104//Hs.159899:AC004853

F-HEMBA1000490//Homo sapiens KIAA0118 mRNA, complete cds//1.2e-50:441:78//Hs.154326:D42087

F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970

F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:D13666

F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093

F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646

F-HEMBA1000518

F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881

F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//2.9e-16:132:84//Hs.155871:AA533783

F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:87//Hs.22383:R51067

F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:AA455706

F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080

F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809

F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389

F-HEMBA1000545//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:K00629

F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684

F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729

F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:AB018303

F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977

F-HEMBA1000568//EST//0.12:270:61//Hs.134833:AI091046

F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042

F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681

F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C.elegans]//7.7e-41:217:96//Hs.55084:AA479162

F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:AJ007509

F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7e-27:463:65//Hs.13794:AA203241

F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.0e-68:574:79//Hs.159176:U92019

F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535

F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925

F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333

F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//7.4e-22:166:84//Hs.26252:AA643235

F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:AB014590

F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174

F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582

F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912

F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073

F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878

F-HEMBA1000686

F-HEMBA1000702

F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309

F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850

F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630

F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881

F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491

F-HEMBA1000747

F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568

F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716

F-HEMBA1000773//ESTs//0.56:336:58//Hs.105864:N35801

F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535210

F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300

[illegible]

F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536

F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542

F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367

F-HEMBA1000843

5 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962

F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572

F-HEMBA1000867

F-HEMBA1000869//ESTs//5.1 e-33:166:77//Hs.141186:R99609

F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237

10 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047

F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660

F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154

F-HEMBA1000910//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046

15 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537

F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142

20 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119

F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596

F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:AA609476

25 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide-synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199

F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369

F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161

30 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903

F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775

F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314

F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936

35 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.127338:AB007961

F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132

F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895

F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835

40 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984

F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:AB007937

45 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572

F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970

50 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142

F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515

F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881

F-HEMBA1001052//EST//0.94:149:67//Hs.31216:AI017971

F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159470:U6088

F-HEMBA1001061//EST//0.0001:272:64//Hs.12364:H09132

F-HEMBA1001071//Alpha 1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14426

F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//

F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536

F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542

F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367

F-HEMBA1000843

5 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962

F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572

F-HEMBA1000867

F-HEMBA1000869//ESTs//5.1 e-33:166:77//Hs.141186:R99609

F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237

10 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047

F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660

F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154

15 F-HEMBA1000910//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046

F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537

F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142

20 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119

F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596

F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:AA609476

25 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide-synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199

F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369

F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161

30 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903

F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775

F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314

F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936

35 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.127338:AB007961

F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132

F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895

F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835

40 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984

F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:AB007937

45 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572

F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970

50 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142

F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515

F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881

F-HEMBA1001052//EST//0.94:149:67//Hs.31216:AI017971

F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159470:U0088

F-HEMBA1001071//ESTs//0.00018:18:18//Hs.24821:AA04481

F-HEMBA1001073//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420

F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//

Hs.147802:R71297

F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172

F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248

F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284

F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750

F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497

F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940

F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917

F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747

F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341

F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582

F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457

F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226

F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499

F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463

P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717

F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694

F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748

F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058

F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046

F-HEMBA1001265

F-HEMBA1001281

F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131

F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741

F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219

F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590

F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201

F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873

F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301

F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427

F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013

F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358

F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794

F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074

F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353

F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848

F-HEMBA1001388

F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660

F-HEMBA1001405

F-HEMBA1001405//ESTs//1.5e-11:455:64//Hs.145386:AI253108

F-HEMBA1001407//ESTs//10.53:390:57//Hs.150447:AI017796

F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

Hs.147802:R71297

F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172

F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248

F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284

F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750

F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497

F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940

F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917

F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747

F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341

F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582

F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457

F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226

F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499

F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463

P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717

F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694

F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748

F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058

F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046

F-HEMBA1001265

F-HEMBA1001281

F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131

F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741

F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219

F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590

F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201

F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873

F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301

F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427

F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013

F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358

F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794

F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074

F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353

F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848

F-HEMBA1001388

F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660

F-HEMBA1001398

F-HEMBA1001401//ESTs//1.3e-61:200:60//Hs.46500:AI177780

F-HEMBA1001404//ESTs//1.3e-61:200:60//Hs.50447:AI017780

F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

F-HEMBA1001413

F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605

F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040

F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726

5 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053

F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031

F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:AA573499

10 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666

F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107

F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412

F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390

15 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144

F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451

F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219

F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054

20 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:M19503

F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902

F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869

F-HEMBA1001526

25 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476

F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580

F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652

F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205

30 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449

F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184

F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228

35 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918

F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210

F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400

F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870

40 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536

F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899

F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204

F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560

45 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283

F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121

F-HEMBA1001661

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943

50 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.158095:AB007953

F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788

F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060

F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760

F-HEMBA1001703

F-HEMBA1001704//ESTs//8.4e-56:255:56//Hs.125346:AI302837

F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114

F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-

F-HEMBA1001413

F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605

F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040

F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726

5 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053

F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031

F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:AA573499

10 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666

F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107

F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412

F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390

15 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144

F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451

F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219

F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054

20 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:M19503

F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902

F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869

F-HEMBA1001526

25 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476

F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580

F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652

F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205

30 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449

F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184

F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228

35 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918

F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210

F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400

F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870

40 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536

F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899

F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204

F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560

45 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283

F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121

F-HEMBA1001661

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943

50 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.158095:AB007953

F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788

F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060

F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760

55 F-HEMBA1001709//EST//1.1e-11:100:100//Hs.136747:AA749210

F-HEMBA1001710//EST//1.1e-11:100:100//Hs.136747:AA749210

F-HEMBA1001711//EST//1.1e-11:100:100//Hs.136747:AA749210

F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-

vegicus//3.0e-30:195:92//Hs.132948:AA194452  
 F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554  
 F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197  
 F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363  
 5 F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415  
 F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250  
 F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924  
 F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328  
 F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:  
 10 N41598  
 F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622  
 F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:  
 AB007943  
 F-HEMBA1001791  
 15 F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570  
 F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817  
 F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233  
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.-5e-175:809:98//Hs.  
 118164:AB007969  
 20 F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305  
 F-HEMBA1001815  
 F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.  
 158174:U66561  
 F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845  
 25 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:  
 AF064244  
 F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:  
 AF071309  
 F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078  
 30 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.I55243:N70293  
 F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324  
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:  
 AB014517  
 F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121  
 35 F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
 PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141922  
 F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036  
 F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.  
 158095:AB007953  
 40 F-HEMBA1001896  
 F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346  
 F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633  
 F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:  
 200:62//Hs.9573:AF027302  
 45 F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511  
 F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141  
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:  
 855:99//Hs.154934:AF000145  
 F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295  
 50 F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221  
 F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882  
 F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943  
 F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360  
 F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.000000:  
 25674:AI141922  
 F-HEMBA1001962//ESTs, Weakly similar to LBR [Hs]//12.5492:AA93889  
 F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708  
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/

vegicus//3.0e-30:195:92//Hs.132948:AA194452

F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554

F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197

F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363

5 F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415

F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250

F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924

F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328

10 F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:N41598

F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622

F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:AB007943

F-HEMBA1001791

15 F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570

F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817

F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.-5e-175:809:98//Hs.118164:AB007969

20 F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305

F-HEMBA1001815

F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.158174:U66561

F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845

25 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:AF064244

F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:AF071309

F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078

30 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293

F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:AB014517

F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121

35 F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141922

F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036

F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.158095:AB007953

40 F-HEMBA1001896

F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346

F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633

F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302

45 F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511

F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145

F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295

50 F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221

F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882

F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943

F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360

F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//Hs.25671:AF100041

F-HEMBA1001962//ESTs//0.0001:289:59//Hs.125492:AA938893

F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477706

F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/

Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178

F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732

F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100

F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581

F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487

F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582

F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426

F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907

F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827

F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057

F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776

F-HEMBA1002084

F-HEMBA1002092

F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832

F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276

F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973

F-HEMBA1002119

F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802

F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393

F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980

F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263

F-HEMBA1002151

F-HEMBA1002153//EST//10.014:328:60//Hs.149115:AI244695

F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976

F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965

F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590

F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219

F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245

F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141

F-HEMBA1002189//EST//5.1 e-24:193:81//Hs.163161:AA778363

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589

F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970

F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696

F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767

F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281

F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957

F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394

F-HEMBA1002237//EST//0.044:1 37:66//Hs.144448:AA812455

F-HEMBA1002241

F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936

F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420

F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445

F-HEMBA1002271//EST//0.00011:233:65//Hs.125552:AA884141

F-HEMBA1002321//Homo sapiens x-rayed low-density lipoprotein receptor mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936

F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178

F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732

F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100

F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581

F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487

F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582

F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426

F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907

F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827

F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057

F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776

F-HEMBA1002084

F-HEMBA1002092

F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832

F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276

F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973

F-HEMBA1002119

F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802

F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393

F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980

F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263

F-HEMBA1002151

F-HEMBA1002153//EST//10.014:328:60//Hs.149115:AI244695

F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976

F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965

F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590

F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219

F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245

F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141

F-HEMBA1002189//EST//5.1 e-24:193:81//Hs.163161:AA778363

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589

F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970

F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696

F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767

F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281

F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957

F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394

F-HEMBA1002237//EST//0.044:1 37:66//Hs.144448:AA812455

F-HEMBA1002241

F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936

F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420

F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445

F-HEMBA1002268

F-HEMBA1002321//Homo sapiens 1.5 kb cDNA, low-density lipoprotein receptor-related protein 1 (LRP1) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936

F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087  
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314  
 F-HEMBA10023481/EST//1.0e-19:285:70//Ms.121860:AA776692  
 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996  
 5 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563  
 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216  
 F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144  
 F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954  
 10 F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141  
 F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289  
 F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561  
 15 F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490  
 F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160  
 F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783  
 20 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912  
 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508  
 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:93//Hs.6189:AB011133  
 F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235  
 F-HEMBA1002495  
 25 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161  
 F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173  
 F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080  
 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972  
 30 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795  
 F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951  
 F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219  
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903  
 35 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875  
 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162  
 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205  
 F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905  
 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587  
 40 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132  
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363  
 45 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169  
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351  
 50 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334  
 F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886  
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390  
 F-HEMBA1002651  
 F-HEMBA1002652//EST//1.6e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002661//Human LINE-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503

F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087  
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314  
 F-HEMBA10023481/EST//1.0e-19:285:70/Ms.121860:AA776692  
 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996  
 5 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563  
 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216  
 F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144  
 F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954  
 10 F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141  
 F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289  
 F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561  
 15 F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490  
 F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160  
 F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783  
 20 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912  
 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508  
 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:93//Hs.6189:AB011133  
 F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235  
 F-HEMBA1002495  
 25 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161  
 F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173  
 F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080  
 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972  
 30 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795  
 F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951  
 F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219  
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903  
 35 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875  
 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162  
 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205  
 F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905  
 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587  
 40 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132  
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363  
 45 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169  
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351  
 50 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334  
 F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886  
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390  
 F-HEMBA1002651  
 F-HEMBA1002652//EST//1.6e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503

F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497

F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368

F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457

5 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601//Hs.124161:AF065164

F-HEMBA10026961//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221

10 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924

F-HEMBA1002712

F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800

F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521

15 F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867

F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596

F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372

F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786

20 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126

F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947

25 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809

F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392

F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326

F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756

F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938

30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185

F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744

F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119

F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904

35 F-HEMBA1002833

F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550

F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823

F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730

40 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429

F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679

F-HEMBA1002921

F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001

F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915

45 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148

F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053

F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703

50 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460

F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925

F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099

F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092

F-HEMBA1002971//ESTs//3.5e-27:140:81//Hs.61170:AA45421

F-HEMBA1002971//ESTs//3.5e-27:140:81//Hs.61170:AA45421

F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4, //1.5e-37:247:89//Hs.188:L20971

F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497

F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368

F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457

5 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601//Hs.124161:AF065164

F-HEMBA10026961//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221

10 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924

F-HEMBA1002712

F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800

F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521

15 F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867

F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596

F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372

F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786

20 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126

F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947

25 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809

F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392

F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326

F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756

F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938

30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185

F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744

F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119

F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904

35 F-HEMBA1002833

F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550

F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823

F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730

40 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429

F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679

F-HEMBA1002921

F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001

F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915

45 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148

F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053

F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703

50 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460

F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925

F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099

F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092

F-HEMBA1002971//ESTs//0.50:100:81//Hs.141770:AA45421

F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4

//1.5e-37:247:89//Hs.188:L20971

F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564

F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525

F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219

5 F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486

F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080

F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454

F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003

F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.I05907:AA186514

10 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182

F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438

F-HEMBA1003067

15 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164

F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865

F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454

F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461

F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881

20 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721

F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872

F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721

F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802

25 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575

F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314

F-HEMBA1003136

F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279

F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670

30 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.I41874:AB014588

F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740

F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.II8831:AA211895

35 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523

F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135

F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412

F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080

F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765

40 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784

F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310

F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012

F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.I32206:AF039694

45 F-HEMBA1003250

F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292

F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991

F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020

50 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864

F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662

F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.8e-167:722:98//Hs.I41874:AB014588

F-HEMBA1003296//EST//1.4e-11:171:83//Hs.I41874:AB014588

F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160

F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.I05486:AA521012

F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564

F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525

F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219

5 F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486

F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080

F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454

F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003

F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.I05907:AA186514

10 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182

F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438

F-HEMBA1003067

15 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164

F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865

F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454

F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461

F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881

20 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721

F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872

F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721

F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802

25 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575

F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314

F-HEMBA1003136

F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279

F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670

30 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.I41874:AB014588

F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740

F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.II8831:AA211895

35 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523

F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135

F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412

F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080

F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765

40 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784

F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310

F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012

F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.I32206:AF039694

45 F-HEMBA1003250

F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292

F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991

F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020

50 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864

F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662

F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-127:331:58//Hs.I321106

F-HEMBA1003286//ESTs//0.047:164:64//Hs.94448:AA770160

F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160

F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.I05486:AA521012

- F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872
- F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459
- F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254
- 5 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003330
- F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329
- F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLf, GCDH, CRTc, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092
- 10 F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159
- F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819
- F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637
- F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017
- F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552
- 15 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488
- F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813
- F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959
- F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309
- F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546
- 20 F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962
- F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058896
- F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378
- F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632
- 25 F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578
- F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600
- F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443
- F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067
- F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811
- 30 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559
- F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311
- F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833
- F-HEMBA1003556
- F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122
- 35 F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327
- F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113
- F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972
- F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546
- 40 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232
- F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285
- F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405
- F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827
- 45 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916
- F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782
- F-HEMBA1003617//Homo sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344
- F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954
- 50 F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750
- F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159
- F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591
- F-HEMBA1003640//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003641//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003642//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003643//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003644//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003645//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003646//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003647//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003648//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003649//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003650//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003651//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003652//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003653//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003654//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003655//EST//0.00023:128:67//Hs.126467:AA913328
- F-HEMBA1003656//EST//0.00023:128:67//Hs.126467:AA913328

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872

F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459

F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254

F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328

F-HEMBA1003330

F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329

F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLf, GCDH, CRTc, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092

F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159

F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819

F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637

F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017

F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552

F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488

F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813

F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959

F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309

F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546

F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962

F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696

F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378

F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632

F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578

F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600

F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443

F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067

F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811

F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559

F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311

F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833

F-HEMBA1003556

F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122

F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327

F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113

F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972

F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546

F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232

F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285

F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405

F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827

F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916

F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782

F-HEMBA1003617//Homo sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344

F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954

F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750

F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159

F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591

F-HEMBA1003640//EST//0.00023:128:67//Hs.126467:AA913328

F-HEMBA1003644

F-HEMBA1003648

F-HEMBA1003656

F-HEMBA1003662

F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381

F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906

F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204

F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]/1.6e-100:478:98//Hs.118866:AI017072

F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691

F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187

F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116

F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995

F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760

F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317

F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921

F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839

F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503

F-HEMBA1003742//Homo sapiens chromosome 19, cosmid

R31180//0.16:242:62//Hs.153325:AC005390

F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946

F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984

F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920

F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]/1.7e-24:224:81//Hs.18171:AA524327

F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172

F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064

F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815

F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239

F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108

F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516

F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220

F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/3.8e-40:151:88//Hs.139007:H74314

F-HEMBA1003856//ESTs//8.6e-53286:95//Hs.116645:AI005167

F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367

F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621:U52840

F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002

F-HEMBA1003880

F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295

F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]/1.2e-49:295:92//Hs.114673:W72675

F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236

F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097

F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI032875

F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389

F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562

F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]/0.0029:222:61//Hs.144236:W52380

F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055

F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580

F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/2.1e-44:243:76//Hs.91146:N73230

F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567

F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965

F-HEMBA1003977

F-HEMBA1003985//ESTs//7.8e-07:60:100//Hs.66058:AA424456

F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456

F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//

F-HEMBA1003662

F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381

F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906

F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204

5 F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]/1.6e-100:478:98//Hs.118866:AI017072

F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691

F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187

F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116

10 F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995

F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760

F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317

F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921

F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839

15 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503

F-HEMBA1003742//Homo sapiens chromosome 19, cosmid

R31180//0.16:242:62//Hs.153325:AC005390

F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946

20 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984

F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920

F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]/1.7e-24:224:81//Hs.18171:AA524327

F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172

F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064

25 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815

F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239

F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108

F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721

30 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516

F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220

F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/3.8e-40:151:88//Hs.139007:H74314

F-HEMBA1003856//ESTs//8.6e-53286:95//Hs.116645:AI005167

35 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367

F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621:U52840

F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002

F-HEMBA1003880

40 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295

F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]/1.2e-49:295:92//Hs.114673:W72675

F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236

F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097

45 F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI032875

F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389

F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562

F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]/0.0029:222:61//Hs.144236:W52380

F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055

50 F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580

F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/2.1e-44:243:76//Hs.91146:N73230

F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567

F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965

F-HEMBA1003977

F-HEMBA1003985//ESTs//1.1e-11:165:74//Hs.54632:AA976236

F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456

F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//



0.022:349:58//Hs.104640:AF000561

F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468

F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493

F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573

5 F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721

F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.15519:AB018315

F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930

F-HEMBA1004042//EST//0.00088:272:6//Hs.155763:AI312281

10 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA584160

F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315

F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435

15 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.46328:D87942

F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426

F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107

F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713

20 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.46468:U45984

F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957

F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064

F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759

F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260

25 F-HEMBA1004143

F-HEMBA1004146

F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056

F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:AB018341

30 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855

F-HEMBA1004199

F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427

F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.2e-35:205:94//Hs.10092:AI189282

35 F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040

F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748

F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514

F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156:67//Hs.163588:AI073878

F-HEMBA1004238

40 F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571

F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522

F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.56205:U96876

F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112

45 F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490:77//Hs.141874:AB014588

F-HEMBA1004272

F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444

F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//Hs.155313:AB002331

50 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364:56//Hs.118738:AB018343

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:99//Hs.101766:AF022795

F-HEMBA1004289

F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484

F-HEMBA1004312//ESTs//0.53:253:59//Hs.111898:AI336310

F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//Hs.69740:U09367

F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532

F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627:U35612

F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062

F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888

F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606  
F-HEMBA1004341

F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686:D89667

F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968

F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376

F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928

F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800

F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019

F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250

F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818

F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199

F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:AI246426

F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531

F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219

F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080

F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606

F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984

F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450

F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600

F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431

F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503

F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492

F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800

F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416

F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381

F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552

F-HEMBA1004554

F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331

F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802

F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825

F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF010238

F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661

F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:1170370

F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606

F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198

F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178

F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416

F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891

F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780

F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522

F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083

F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796

F-HEMBA1004670//Membrane protein 1006 (MEMP1006) mRNA

F-HEMBA1004672//ESTs//1.4e-35:144:35//Hs.86237:AA20614

F-HEMBA1004693//ESTs//0.00033:301:95//Hs.159066:AI093254

F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821

F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627:U35612

F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062

F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888

F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606  
F-HEMBA1004341

F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686:D89667

F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968

F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376

F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928

F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800

F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019

F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250

F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818

F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199

F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:AI246426

F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531

F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219

F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080

F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606

F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984

F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450

F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600

F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431

F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503

F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492

F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800

F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416

F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381

F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552

F-HEMBA1004554

F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331

F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802

F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825

F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF010238

F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661

F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:1170370

F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606

F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198

F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178

F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416

F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891

F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780

F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522

F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083

F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796

F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:61

F-HEMBA1004671//ESTs//1.1e-11:114:10//Hs.86201:AA20614

F-HEMBA1004693//ESTs//1.1e-15:311:95//Hs.159066:AI093251

F-HEMBA1004697//H sapiens mRNA for ribosomal protein L16a homologue//0.64:313:61//Hs.118578:X80821

- F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892  
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515  
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019  
 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903  
 5 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909  
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515  
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004  
 10 F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503  
 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813  
 F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504  
 F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626  
 15 F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.I53563:AF011333  
 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082  
 F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060  
 F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.I55657:M61120  
 20 F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503  
 F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139  
 F-HEMBA1004771  
 F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235  
 25 F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106  
 F-HEMBA1004795  
 F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952  
 F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971  
 30 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042  
 F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646  
 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481  
 F-HEMBA1004847//ESTs//2.1 e-09:66:98//Hs.158161:AA312511  
 35 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601  
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150  
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987  
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077  
 40 F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633  
 F-HEMBA1004889//Growth arrest-specific V//0.20:146:68//Hs.65029:L13698  
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304  
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106  
 F-HEMBA1004918//EST//0.78:122:61//Hs.I45491:AI254348  
 45 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172  
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947  
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959  
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331  
 50 F-HEMBA1004934  
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981  
 F-HEMBA1004954//ESTs//0.04:404:60//Hs.11177:AA417813  
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478  
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274  
 55 F-HEMBA1004972  
 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892  
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515  
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019  
 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903  
 5 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909  
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515  
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004  
 10 F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503  
 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813  
 F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504  
 F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626  
 15 F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.I53563:AF011333  
 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082  
 F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060  
 F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.I55657:M61120  
 20 F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503  
 F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139  
 F-HEMBA1004771  
 F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235  
 25 F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106  
 F-HEMBA1004795  
 F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952  
 F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971  
 30 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042  
 F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646  
 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481  
 F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511  
 35 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601  
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150  
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987  
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077  
 40 F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633  
 F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698  
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304  
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106  
 F-HEMBA1004918//EST//0.78:122:61//Hs.I45491:AI254348  
 45 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172  
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947  
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959  
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331  
 50 F-HEMBA1004934  
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981  
 F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813  
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478  
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274  
 F-HEMBA1004970  
 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

- F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013  
 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750  
 F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589  
 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026  
 5 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429  
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356  
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548  
 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560  
 10 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237  
 F-HEMBA1005039//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627  
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193  
 15 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802  
 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462  
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587  
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381  
 20 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785  
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105  
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561  
 25 F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916  
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304  
 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106  
 F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875  
 30 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021  
 F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216  
 F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914  
 F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197  
 F-HEMBA1005202  
 35 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436  
 F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547  
 F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081  
 F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302  
 F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144  
 40 F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs.128744:AI191922  
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896  
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157  
 45 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380  
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777  
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018  
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232  
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219  
 50 F-HEMBA1005311  
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516  
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615  
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117  
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68722  
 55 F-HEMBA1005338//Homo sapiens mRNA for matrix metalloproteinase 1 (MMP-1) (clone pZ-30)//5.7e-100:500:88//Hs.151689:U09414  
 F-HEMBA1005339//EST//1.2e-68//Hs.149508:AA485703  
 F-HEMBA1005359//Zinc finger protein 107 (clone pZ-30)//5.7e-100:500:88//Hs.151689:U09414  
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265

F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013  
 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750  
 F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589  
 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026  
 5 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429  
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356  
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548  
 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560  
 10 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237  
 F-HEMBA1005039//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627  
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193  
 15 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802  
 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462  
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587  
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381  
 20 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785  
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105  
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561  
 25 F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916  
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304  
 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106  
 F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875  
 30 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021  
 F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216  
 F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914  
 F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197  
 F-HEMBA1005202  
 35 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436  
 F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547  
 F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081  
 F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302  
 F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144  
 40 F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs.128744:AI191922  
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896  
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157  
 45 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380  
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777  
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018  
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232  
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219  
 50 F-HEMBA1005311  
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516  
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615  
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117  
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68700  
 55 F-HEMBA1005338//Homo sapiens mRNA for p115, a protein of the p53 pathway  
 F-HEMBA1005353//EST//0.00011:111:68//Hs.108508:AA485701  
 F-HEMBA1005359//Zinc finger protein 107 (clone pRZ-30)//5.7e-100:500:88//Hs.151689:U09414  
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265

AF071787

F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905

F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452

5 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053

F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448

F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:N25951

10 F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:AI033807

F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513

F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347

F-HEMBA1005411

15 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248

F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323

F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687

F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783

F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107

20 F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368

F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503

F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219

25 F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694

F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029

F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957

30 F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911

F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353

F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220

35 F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693

F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575

F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280

40 F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219

F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471

F-HEMBA1005530

45 F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376

F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461

F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903

F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257

F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507

50 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932

F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873

F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538

F-HEMBA1005582

F-HEMBA1005583

F-HEMBA1005588//ESTs, Weakly similar to No definition line found [H.sapiens]//1.0e-10:100:100//Hs.100000:U00000

F-HEMBA1005593//S-ADENOSYL METHIONINE SYNTHETASE [EC 2.3.1.6]//Hs.100000:U00000

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

AF071787

F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905

F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452

5 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053

F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448

F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:N25951

10 F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:AI033807

F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513

F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347

F-HEMBA1005411

15 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248

F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323

F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687

F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783

F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107

20 F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368

F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503

F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219

25 F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694

F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029

F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957

30 F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911

F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353

F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220

35 F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693

F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575

F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280

40 F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219

F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471

F-HEMBA1005530

F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376

45 F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461

F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903

F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257

F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507

50 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932

F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873

F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538

F-HEMBA1005582

F-HEMBA1005583

F-HEMBA1005584

F-HEMBA1005593//S-ADENOSYL METHIONINE SYNTHETASE [EC 2.3.1.6] mRNA

ORMS//0.54:439:59//Hs.2137:D49357

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609  
 F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982  
 F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280  
 5 F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845  
 F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535  
 F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734  
 F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199  
 10 F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956  
 F-HEMBA1005666  
 F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142  
 F-HEMBA1005679//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629  
 15 F-HEMBA1005680  
 F-HEMBA1005685  
 F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406  
 F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678  
 20 F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143  
 F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-20:151:88//Hs.77393:D14697  
 F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754  
 F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024  
 25 F-HEMBA1005755//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627  
 F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219  
 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141  
 F-HEMBA10058131//ESTs//0.012:209:63//Hs.113365:R77747  
 F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346  
 30 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577  
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788  
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503  
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204  
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150  
 35 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953  
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097  
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984  
 40 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766  
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081  
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006  
 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880  
 45 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588  
 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883  
 F-HEMBA1005963  
 F-HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516  
 50 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530  
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526  
 F-HEMBA1006002  
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151  
 F-HEMBA1006006  
 F-HEMBA1006007  
 F-HEMBA1006036//Homo sapiens h-puV (MERV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080  
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609  
 F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982  
 F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280  
 5 F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845  
 F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535  
 F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734  
 F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199  
 10 F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956  
 F-HEMBA1005666  
 F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142  
 F-HEMBA1005679//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629  
 15 F-HEMBA1005680  
 F-HEMBA1005685  
 F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406  
 F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678  
 20 F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143  
 F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-20:151:88//Hs.77393:D14697  
 F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754  
 F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024  
 25 F-HEMBA1005755//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627  
 F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219  
 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141  
 F-HEMBA10058131//ESTs//0.012:209:63//Hs.113365:R77747  
 F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346  
 30 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577  
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788  
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503  
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204  
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150  
 35 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953  
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097  
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984  
 40 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766  
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081  
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006  
 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880  
 45 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588  
 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883  
 F-HEMBA1005963  
 F-HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516  
 50 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530  
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526  
 F-HEMBA1006002  
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein ID melanogaster//0.98:187:61//Hs.5184:AA700151  
 F-HEMBA1006006  
 F-HEMBA1006036//Homo sapiens PVRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080  
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422

F-HEMBA1006081

F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788

F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313

5 F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799

F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741

F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968

F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222

F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372

10 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734

F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881

F-HEMBA1006155

F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575

F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627

15 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117

F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540

F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557

F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046

F-HEMBA1006252

20 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706

F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:AB018341

F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631

F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140

25 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770

F-HEMBA1006283

F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964

F-HEMBA1006291

F-HEMBA1006293

30 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285

F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174

F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350

F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789

35 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142

F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220

F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287

F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244

40 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026

F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233

F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922

45 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531

F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503

F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477

F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881

F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830

50 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835

F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264

F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194

F-HEMBA1006445

F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889

F-HEMBA1006461//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]

F-HEMBA1006464

F-HEMBA1006471//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]

F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257

F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422

F-HEMBA1006081

F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788

F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313

5 F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799

F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741

F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968

F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222

F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372

10 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734

F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881

F-HEMBA1006155

F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575

F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627

15 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117

F-HEMBA1006198//ESTs//0.017:133 :67//Hs.142168:AA292540

F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557

F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046

F-HEMBA1006252

20 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706

F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:AB018341

F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631

F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140

25 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770

F-HEMBA1006283

F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964

F-HEMBA1006291

F-HEMBA1006293

30 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285

F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174

F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350

F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789

35 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142

F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220

F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287

F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244

40 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026

F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233

F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922

45 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531

F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503

F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477

F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881

F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830

50 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835

F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264

F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194

F-HEMBA1006445

F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889

55 F-HEMBA1006461//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257

F-HEMBA1006462

F-HEMBA1006471//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257

F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257

AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625

F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389

F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072

F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566

F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185

F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002

F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs21301:AF093419

F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638

F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898

F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425

F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136

F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:AI346522

F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479

F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778

F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219

F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295

F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862

F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875

F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331

F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589

F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185

F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003

F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282

F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189

F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065

F-HEMBA1006676

F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575

F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145

F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198

F-HEMBA1006708

F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545

F-HEMBA1006717//ESTs//12.6e-31:286:78//Hs.55573:W37226

F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105

F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087

F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129707:AF035587

F-HEMBA1006758//Homo sapiens KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087

F-HEMBA1006767//ESTs//1.8e-26:172//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625

F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389

F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072

F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566

F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185

F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002

F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs21301:AF093419

F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638

F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898

F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425

F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136

F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:AI346522

F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479

F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778

F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219

F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295

F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862

F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875

F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331

F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589

F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185

F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003

F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282

F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189

F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065

F-HEMBA1006676

F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575

F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145

F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198

F-HEMBA1006708

F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545

F-HEMBA1006717//ESTs//12.6e-31:286:78//Hs.55573:W37226

F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105

F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087

F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds

F-HEMBA1006755//EST//1.1e-10:100:60//Hs.154326:D42087

F-HEMBA1006758//Human mRNA for KIAA0321 protein, complete cds//1.1e-10:100:60//Hs.154326:D42087

F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

- F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250  
 F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798  
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503  
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298  
 5 F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMO-SOME III [*C.elegans*]//4.8e-110:523:98//Hs.125790:AA287723  
 F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551  
 F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624  
 F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970  
 10 F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327  
 F-HEMBA1006865  
 F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [*Saccharomyces cerevisiae*]//2.4e-61:311:97//Hs.127793:W25938  
 F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [*Saccharomyces cerevisiae*]//9.1e-128:805:87//Hs.32376:AA758214  
 15 F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592  
 F-HEMBA1006914//EST//0.065:366:621//Hs.162914:AA666199  
 F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989  
 F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258  
 20 F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539  
 F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712  
 F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382  
 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:AJ010841  
 25 F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633  
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.14934:AF004828  
 F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase//1.9e-79:447:89//Hs.75268:X74570  
 30 F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968  
 F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723  
 F-HEMBA1007002  
 F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282  
 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:70//Hs.43003:AF035812  
 35 F-HEMBA1007045  
 F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659  
 F-HEMBA1007052  
 F-HEMBA1007062  
 40 F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212  
 F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845  
 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:M74002  
 F-HEMBA1007080  
 45 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432  
 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:57//Hs.3828:U49260  
 F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595  
 F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354  
 50 F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182  
 F-HEMBA1007129  
 F-HEMBA1007147//ESTs//3.2e-07:235:641//Hs.124813:W46172  
 F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136  
 F-HEMBA1007151  
 55 F-HEMBA1007174//EST//1.0:59:72//Hs.113400:R39282  
 F-HEMBA1007183//ESTs, Moderately similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [*Saccharomyces cerevisiae*]//2.4e-61:311:97//Hs.127793:W25938  
 F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250  
 F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798  
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503  
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298  
 5 F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMO-  
 SOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723  
 F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551  
 F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624  
 F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970  
 10 F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327  
 F-HEMBA1006865  
 F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938  
 F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC  
 15 REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214  
 F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592  
 F-HEMBA1006914//EST//0.065:366:621//Hs.162914:AA666199  
 F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989  
 F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258  
 20 F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539  
 F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712  
 F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382  
 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:  
 AJ010841  
 25 F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633  
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.  
 14934:AF004828  
 F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase//1.9e-79:447:89//  
 Hs.75268:X74570  
 30 F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968  
 F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723  
 F-HEMBA1007002  
 F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282  
 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:  
 35 70//Hs.43003:AF035812  
 F-HEMBA1007045  
 F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659  
 F-HEMBA1007052  
 F-HEMBA1007062  
 40 F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212  
 F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845  
 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:  
 M74002  
 F-HEMBA1007080  
 45 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432  
 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:  
 57//Hs.3828:U49260  
 F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595  
 F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354  
 50 F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182  
 F-HEMBA1007129  
 F-HEMBA1007147//ESTs//3.2e-07:235:641//Hs.124813:W46172  
 F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136  
 F-HEMBA1007151  
 55 F-HEMBA1007174//ESTs, Moderately similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938  
 F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:  
 D86987  
 F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252  
 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197:  
 5 AB018340  
 F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.  
 82314:M31642  
 F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204  
 F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575  
 10 F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749:  
 U13695  
 F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836  
 F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475  
 F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529  
 15 F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637  
 F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062  
 F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615  
 F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506  
 F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634  
 20 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241  
 F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.5e-09:144:76//Hs.20597:  
 W58370  
 F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130  
 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006  
 25 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561  
 F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568  
 F-HEMBA1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073  
 F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.  
 83428:M58603  
 30 F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307  
 F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392  
 F-HEMBA1000030//H.sapiens mRNA for cyclin II//1.3e-10:525:62//Hs.3232:Z46788  
 F-HEMBA1000036  
 F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:  
 35 98//Hs.20815:AF084928  
 F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358  
 F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319  
 F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131  
 F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717  
 40 F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503  
 F-HEMBA1000055//ESTs//0.0017:289:62//Hs.125755:AA286923  
 F-HEMBA1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304  
 F-HEMBA1000083  
 F-HEMBA1000089//EST//0.0016:192:661//Hs.137093:AA917621  
 45 F-HEMBA1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645  
 F-HEMBA1000103//Human kpni repeat mna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627  
 F-HEMBA1000113//EST//4.6e-23:221:76//Hs.142065:AA173763  
 F-HEMBA1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521  
 F-HEMBA1000136//ESTs//112.3e-101:507:96//Hs.12659:AA195207  
 50 F-HEMBA1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044  
 F-HEMBA1000144//EST//4.5e-52:298:91//Hs.149580:AI281881  
 F-HEMBA1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715  
 F-HEMBA1000175//EST//1.0:101:65//Hs.162898:AA659646  
 F-HEMBA1000198//EST//0.99:179:56//Hs.116880:AA662457  
 F-HEMBA1000217//ESTs//3.4e-06:81:66//Hs.121151:U66277  
 F-HEMBA1000218//EST//0.11:136:63//Hs.134683:AI092013

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363: D86987

F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252

F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197: AB018340

F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs. 82314:M31642

F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204

F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575

F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749: U13695

F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836

F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475

F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529

F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637

F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062

F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615

F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506

F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634

F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241

F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]/3.5e-09:144:76//Hs.20597: W58370

F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130

F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006

F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561

F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568

F-HEMBA1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073

F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs. 83428:M58603

F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307

F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392

F-HEMBA1000030//H.sapiens mRNA for cyclin II//1.3e-10:525:62//Hs.3232:Z46788

F-HEMBA1000036

F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450: 98//Hs.20815:AF084928

F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358

F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319

F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131

F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717

F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503

F-HEMBA1000055//ESTs//0.0017:289:62//Hs.125755:AA286923

F-HEMBA1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304

F-HEMBA1000083

F-HEMBA1000089//EST//0.0016:192:661//Hs.137093:AA917621

F-HEMBA1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645

F-HEMBA1000103//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627

F-HEMBA1000113//EST//4.6e-23:221:76//Hs.142065:AA173763

F-HEMBA1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521

F-HEMBA1000136//ESTs//1.2e-101:507:96//Hs.12659:AA195207

F-HEMBA1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044

F-HEMBA1000144//EST//4.5e-52:298:91//Hs.149580:AI281881

F-HEMBA1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715

F-HEMBA1000175//EST//1.0:101:65//Hs.162898:AA659646

F-HEMBA1000198//EST//0.99:179:56//Hs.116880:AA662457

F-HEMBA1000217

F-HEMBA1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277

F-HEMBA1000218//EST//0.11:136:63//Hs.134683:AI092013

- F-HEM BB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962  
 F-HEM BB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612  
 F-HEM BB1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483  
 5 F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981//Hs.151411:AF075587  
 F-HEM BB1000258//EST//0.0091:325:60//Hs.97533:AA435884  
 F-HEM BB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968  
 F-HEM BB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930  
 10 F-HEM BB1000272//ESTs//1.3e-93:440:99//Hs.I09224:N46684  
 F-HEM BB1000274//ESTs//0.41:221:65//Hs.71990:AA151796  
 F-HEM BB1000284//EST//0.00024:108:73//Hs.100725:F13689  
 F-HEM BB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574  
 F-HEM BB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:AB018326  
 15 F-HEM BB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787  
 F-HEM BB1000318//EST//0.014:184:61//Hs.155758:AI311870  
 F-HEM BB1000335//EST//0.99:187:63//Hs.137424:AA243729  
 F-HEM BB1000336//EST//1.0:209:63//Hs.150410:AI003611  
 20 F-HEM BB1000337//EST//0.086:133:66//Hs.128207:AA972330  
 F-HEM BB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127  
 F-HEM BB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:761//Hs.155464:AF088219  
 F-HEM BB1000341  
 F-HEM BB1000343//EST//0.66:163:63//Hs.150822:AI302729  
 25 F-HEM BB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874  
 F-HEM BB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:AI420970  
 F-HEM BB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934  
 F-HEM BB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348  
 F-HEM BB1000391//ESTs//0.033:237:64//Hs.135289:AI092963  
 30 F-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642  
 F-HEM BB1000402//EST//0.013:291:59//Hs.149191:AI246155  
 F-HEM BB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEM BB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEM BB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735:AF010144  
 35 F-HEM BB1000438//ESTs//0.073:446:58//Hs.134632:AI223429  
 F-HEM BB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEM BB1000449//EST//5.5e-21:356:671//Hs.157848:AI362501  
 F-HEM BB1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 40 F-HEM BB1000472  
 F-HEM BB1000480//EST//0.98:83:71//Hs.146462:AI124898  
 F-HEM BB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEM BB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560  
 F-HEM BB1000491  
 45 F-HEM BB1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEM BB1000510//Glucocorticoid receptor alpha (alternative products)//1.6e-46:409:77//Hs.102761:U25029  
 F-HEM BB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEM BB1000523//ESTs//0.69:332:59//Hg.106845:W19543  
 F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710  
 50 F-HEM BB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/7.7e-31:554:67//Hs.157142:U85996  
 F-HEM BB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953  
 F-HEM BB1000564  
 F-HEM BB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

- F-HEM BB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962  
 F-HEM BB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612  
 F-HEM BB1000244//ESTs//3.2e-15:139:81//HS.134549:AI078483  
 5 F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981//Hs.151411:AF075587  
 F-HEM BB1000258//EST//0.0091:325:60//Hs.97533:AA435884  
 F-HEM BB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968  
 F-HEM BB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930  
 10 F-HEM BB1000272//ESTs//1.3e-93:440:99//Hs.I09224:N46684  
 F-HEM BB1000274//ESTs//0.41:221:65//Hs.71990:AA151796  
 F-HEM BB1000284//EST//0.00024:108:73//Hs.100725:F13689  
 F-HEM BB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574  
 F-HEM BB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:AB018326  
 15 F-HEM BB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787  
 F-HEM BB1000318//EST//0.014:184:61//Hs.155758:AI311870  
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 F-HEM BB1000336//EST//1.0:209:63//Hs.150410:AI003611  
 20 F-HEM BB1000337//EST//0.086:133:66//Hs.128207:AA972330  
 F-HEM BB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127  
 F-HEM BB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:7611Hs.155464:AF088219  
 F-HEM BB1000341  
 F-HEM BB1000343//EST//0.66:163:63//Hs.150822:AI302729  
 25 F-HEM BB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874  
 F-HEM BB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:AI420970  
 F-HEM BB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934  
 F-HEM BB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348  
 F-HEM BB1000391//ESTs//0.033:237:64//Hs.135289:AI092963  
 30 F-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642  
 F-HEM BB1000402//EST//0.013:291:59//Hs.149191:AI246155  
 F-HEM BB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEM BB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEM BB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735AF010144  
 35 F-HEM BB1000438//ESTs//0.073:446:58//Hs.134632:AI223429  
 F-HEM BB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEM BB1000449//EST//5.5e-21:356:671//Hs.157848:AI362501  
 F-HEM BB1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 40 F-HEM BB1000472  
 F-HEM BB1000480//EST//0.98:83:71//Hs.146462:AI124898  
 F-HEM BB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEM BB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560  
 F-HEM BB1000491  
 45 F-HEM BB1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEM BB1000510//Glucocorticoid receptor alpha {alternative products}/1.6e-46:409:77//Hs.102761:U25029  
 F-HEM BB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEM BB1000523//ESTs//0.69:332:59//Hg.106845:W19543  
 F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710  
 50 F-HEM BB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/7.7e-31:554:67//Hs.157142:U85996  
 F-HEM BB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953  
 F-HEM BB1000555  
 F-HEM BB1000556  
 F-HEM BB1000564  
 F-HEM BB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

- F-HEM BB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238  
 F-HEM BB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533  
 F-HEM BB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091  
 5 F-HEM BB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990  
 F-HEM BB1000592//EST//0.0038:51:88//Hs.148022:AI269323  
 F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356  
 F-HEM BB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589  
 F-HEM BB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809  
 10 F-HEM BB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864  
 F-HEM BB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481  
 F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349  
 F-HEM BB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075  
 F-HEM BB1000638//EST//0.0076:92:75//Hs.125496:AA883735  
 15 F-HEM BB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830  
 F-HEM BB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778  
 F-HEM BB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531  
 F-HEM BB1000665//EST//0.44:152:63//Hs.149534:AI280924  
 F-HEM BB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503  
 20 F-HEM BB1000673//ESTs//0.99:177:59//Hs.149864:N80474  
 F-HEM BB1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.73821:M35663  
 F-HEM BB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723  
 F-HEM BB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125  
 25 F-HEM BB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703  
 F-HEM BB1000709//EST//0.99:110:651//Hs.162437:AA577510  
 F-HEM BB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741  
 F-HEM BB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216  
 F-HEM BB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328  
 30 F-HEM BB1000749//EST//3.1e-42:271:871//Hs.162197:AA535216  
 F-HEM BB1000763  
 F-HEM BB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830  
 F-HEM BB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390  
 35 F-HEM BB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876  
 F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:AB014577  
 F-HEM BB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727  
 F-HEM BB1000794//ESTs//0.00098:289:59//Hs.138782:N73572  
 40 F-HEM BB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375  
 F-HEM BB1000810//ESTs//0.038:92:71//Hs.148763:AA66887  
 F-HEM BB1000821//EST//0.94:129:62//Hs.162299:AA555154  
 F-HEM BB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421  
 F-HEM BB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069  
 45 F-HEM BB1000827  
 F-HEM BB1000831  
 F-HEM BB1000835//EST//4.3e-27:201:851//Hs.141451:N29915  
 F-HEM BB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948  
 F-HEM BB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:M19503  
 50 F-HEM BB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238  
 F-HEM BB1000870//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351  
 F-HEM BB1000883//ESTs//0.42:107:67//Hs.154173:AI379823  
 F-HEM BB1000888//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000888//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000890//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000893//EST//0.0079:408:58//Hs.146504:AI129834

F-HEM BB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238  
 F-HEM BB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533  
 F-HEM BB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091  
 5 F-HEM BB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990  
 F-HEM BB1000592//EST//0.0038:51:88//Hs.148022:AI269323  
 F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356  
 F-HEM BB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589  
 F-HEM BB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809  
 10 F-HEM BB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864  
 F-HEM BB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481  
 F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349  
 F-HEM BB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075  
 F-HEM BB1000638//EST//0.0076:92:75//Hs.125496:AA883735  
 15 F-HEM BB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830  
 F-HEM BB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778  
 F-HEM BB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531  
 F-HEM BB1000665//EST//0.44:152:63//Hs.149534:AI280924  
 F-HEM BB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503  
 20 F-HEM BB1000673//ESTs//0.99:177:59//Hs.149864:N80474  
 F-HEM BB1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.73821:M35663  
 F-HEM BB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723  
 F-HEM BB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125  
 25 F-HEM BB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703  
 F-HEM BB1000709//EST//0.99:110:651//Hs.162437:AA577510  
 F-HEM BB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741  
 F-HEM BB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216  
 F-HEM BB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328  
 30 F-HEM BB1000749//EST//3.1e-42:271:871//Hs.162197:AA535216  
 F-HEM BB1000763  
 F-HEM BB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830  
 F-HEM BB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390  
 35 F-HEM BB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876  
 F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:AB014577  
 F-HEM BB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727  
 F-HEM BB1000794//ESTs//0.00098:289:59//Hs.138782:N73572  
 40 F-HEM BB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375  
 F-HEM BB1000810//ESTs//0.038:92:71//Hs.148763:AA66887  
 F-HEM BB1000821//EST//0.94:129:62//Hs.162299:AA555154  
 F-HEM BB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421  
 F-HEM BB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069  
 45 F-HEM BB1000827  
 F-HEM BB1000831  
 F-HEM BB1000835//EST//4.3e-27:201:851//Hs.141451:N29915  
 F-HEM BB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948  
 F-HEM BB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:M19503  
 50 F-HEM BB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238  
 F-HEM BB1000870//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351  
 F-HEM BB1000883//ESTs//0.42:107:67//Hs.154173:AI379823  
 55 F-HEM BB1000887  
 F-HEM BB1000888//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000890//ESTs//0.00091:246:62//Hs.126502:AA913831  
 F-HEM BB1000893//EST//0.0079:408:58//Hs.146504:AI129834

F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875  
 F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984  
 F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049  
 F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468  
 5 F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089  
 F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593  
 F-HEMBB1000947  
 F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942  
 F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938  
 10 F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124  
 F-HEMBB1000981  
 F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569  
 F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713  
 15 F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055  
 F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565  
 F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025  
 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310  
 20 F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247  
 F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970  
 F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:AI291177  
 25 F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721  
 F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586  
 F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518  
 F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219  
 30 F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942  
 F-HEMBB1001063  
 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803  
 F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272  
 F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293  
 35 F-HEMBB1001105//Human BRCA2 region, mRNA sequence  
 CG016//0.30:84:75//Hs.112434:U50529  
 F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800  
 F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062  
 40 F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139  
 F-HEMBB1001119  
 F-HEMBB1001126  
 F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073  
 F-HEMBB1001137  
 45 F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329  
 F-HEMBB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854  
 F-HEMBB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716  
 F-HEMBB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863  
 F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334  
 50 F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183  
 F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129  
 F-HEMBB1001199  
 F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802  
 F-HEMBB1001209//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEMBB1001210//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEMBB1001211//H.sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157  
 F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.

F-HEM BB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875  
 F-HEM BB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984  
 F-HEM BB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049  
 F-HEM BB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468  
 5 F-HEM BB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089  
 F-HEM BB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593  
 F-HEM BB1000947  
 F-HEM BB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942  
 F-HEM BB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938  
 10 F-HEM BB1000975//ESTs//0.78:180:66//Hs.104789:AA417124  
 F-HEM BB1000981  
 F-HEM BB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569  
 F-HEM BB1000991//EST//0.12:125:66//Hs.22945:R43713  
 15 F-HEM BB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055  
 F-HEM BB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565  
 F-HEM BB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025  
 F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310  
 20 F-HEM BB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEM BB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247  
 F-HEM BB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970  
 F-HEM BB1001037//EST//0.0057:192:66//Hs.149987:AI291177  
 25 F-HEM BB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721  
 F-HEM BB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586  
 F-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518  
 F-HEM BB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219  
 30 F-HEM BB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942  
 F-HEM BB1001063  
 F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803  
 F-HEM BB1001096//EST//0.017:154:66//Hs.130403:AA909272  
 F-HEM BB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293  
 35 F-HEM BB1001105//Human BRCA2 region, mRNA sequence  
 CG016//0.30:84:75//Hs.112434:U50529  
 F-HEM BB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800  
 F-HEM BB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062  
 40 F-HEM BB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139  
 F-HEM BB1001119  
 F-HEM BB1001126  
 F-HEM BB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073  
 F-HEM BB1001137  
 45 F-HEM BB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329  
 F-HEM BB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854  
 F-HEM BB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716  
 F-HEM BB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863  
 F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334  
 50 F-HEM BB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183  
 F-HEM BB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129  
 F-HEM BB1001199  
 F-HEM BB1001208//ESTs//0.12:120:68//Hs.130093:AA828800  
 F-HEM BB1001210//EST//0.41:107:60//Hs.88840:AA281441  
 F-HEM BB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157  
 F-HEM BB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.

158241:AB007976

F-HEM BB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:AI378790

F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754

F-HEM BB1001249//EST//0.26:203:63//Hs.140791:AA935909

F-HEM BB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219

F-HEM BB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977

F-HEM BB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828

F-HEM BB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248

F-HEM BB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)//0.39:531:57//Hs.78915:U13045

F-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021

F-HEM BB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890

F-HEM BB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848

F-HEM BB1001302

F-HEM BB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEM BB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

F-HEM BB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219

F-HEM BB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503

F-HEM BB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

F-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222

F-HEM BB1001335

F-HEM BB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135

F-HEM BB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694

F-HEM BB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

F-HEM BB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142

F-HEM BB1001356//EST//0.32:292:59//Hs.135771:AI005648

F-HEM BB1001364

F-HEM BB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

F-HEM BB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219

F-HEM BB1001369//EST//0.17:211:63//Hs.120066:AA707973

F-HEM BB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099

F-HEM BB1001384

F-HEM BB1001387//ESTs//0.61:215:60//Hs.145915:AI342230

F-HEM BB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503

F-HEM BB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988

F-HEM BB1001424//EST//0.20:307:58//Hs.135336:AI049827

F-HEM BB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174

F-HEM BB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175

F-HEM BB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345

F-HEM BB1001443

F-HEM BB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216

F-HEM BB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038

F-HEM BB1001458//EST//1.7e-09:106:83//Hs.141422:N20920

F-HEM BB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

F-HEM BB1001464//EST//0.0001:257:63//Hs.62208:H12380

F-HEM BB1001465//EST//0.0001:257:63//Hs.62208:H12380

F-HEM BB1001466

F-HEM BB1001500//ESTs//6.1e-28:312:74//Hs.18498:N52088

158241:AB007976

F-HEM BB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]/6.7e-103:477:100//Hs.127835:AI378790

F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754

F-HEM BB1001249//EST//0.26:203:63//Hs.140791:AA935909

F-HEM BB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219

F-HEM BB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977

F-HEM BB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)/6.1e-24:146:78//Hs.51187:U82828

F-HEM BB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248

F-HEM BB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)/0.39:531:57//Hs.78915:U13045

F-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]/4.9e-10:91:89//Hs.16606:W81021

F-HEM BB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890

F-HEM BB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]/1.3e-135:654:98//Hs.124217:AA020848

F-HEM BB1001302

F-HEM BB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEM BB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

F-HEM BB1001315//Small inducible cytokine A5 (RANTES)/1.9e-40:355:78//Hs.155464:AF088219

F-HEM BB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503

F-HEM BB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

F-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]/1.0e-48:332:87//Hs.43071:AA206222

F-HEM BB1001335

F-HEM BB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135

F-HEM BB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694

F-HEM BB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

F-HEM BB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142

F-HEM BB1001356//EST//0.32:292:59//Hs.135771:AI005648

F-HEM BB1001364

F-HEM BB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

F-HEM BB1001367//Small inducible cytokine A5 (RANTES)/8.7e-50:326:86//Hs.155464:AF088219

F-HEM BB1001369//EST//0.17:211:63//Hs.120066:AA707973

F-HEM BB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099

F-HEM BB1001384

F-HEM BB1001387//ESTs//0.61:215:60//Hs.145915:AI342230

F-HEM BB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503

F-HEM BB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988

F-HEM BB1001424//EST//0.20:307:58//Hs.135336:AI049827

F-HEM BB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174

F-HEM BB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]/5.5e-153:729:96//Hs.21679:AF034175

F-HEM BB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345

F-HEM BB1001443

F-HEM BB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216

F-HEM BB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038

F-HEM BB1001458//EST//1.7e-09:106:83//Hs.141422:N20920

F-HEM BB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

F-HEM BB1001464//EST//0.0001:257:63//Hs.62208:H12380

F-HEM BB1001482//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.0e-104:114:78:1018300

F-HEM BB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942

F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815

F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735

F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093

F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748

F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306

F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315

F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:AI208240

F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953

F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080

F-HEMBB1001585

F-HEMBB1001586//EST//0.84:132:64//Hs.145264:AI218708

F-HEMBB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289

F-HEMBB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414

F-HEMBB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680

F-HEMBB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314

F-HEMBB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713

F-HEMBB1001635//ESTs//0.92:282:60//Hs.126980:AA934077

F-HEMBB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172

F-HEMBB1001641//EST//0.11:53:81//Hs.112445:AA594279

F-HEMBB1001653//EST//0.91:124:64//Hs.144213:T40480

F-HEMBB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407

F-HEMBB1001668//ESTs//0.94:83:69//Hs.146202:AI252519

F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546

F-HEMBB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496

F-HEMBB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430

F-HEMBB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664

F-HEMBB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398

F-HEMBB1001706

F-HEMBB1001707//EST//0.091:241:60//Hs.136830:AA769219

F-HEMBB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064

F-HEMBB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219

F-HEMBB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578

F-HEMBB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244

F-HEMBB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144

F-HEMBB1001753//ESTs//0.00013:35:100//Hs.139643:H06263

F-HEMBB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077

F-HEMBB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639

F-HEMBB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976

F-HEMBB1001785//EST//0.16:262:60//Hs.162526:AA584102

F-HEMBB1001797//ESTs//0.37:201:63//Hs.91559:AA806370

F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951

F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956

F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017

F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-10:298:63//Hs.122771:U07664

F-HEMBB1001834//TRIM-11/ALIN, complete cds//5.4e-60//Hs.82276:U0919

F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067

F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

- F-HEM BB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942
- F-HEM BB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
- F-HEM BB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735
- 5 F-HEM BB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
- F-HEM BB1001536//ESTs//0.0047:120:68//Hs.144858:R67748
- F-HEM BB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
- 10 F-HEM BB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315
- F-HEM BB1001562//ESTs//0.95:161:61//Hs.145075:AI208240
- F-HEM BB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
- F-HEM BB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080
- 15 F-HEM BB1001585
- F-HEM BB1001586//EST//0.84:132:64//Hs.145264:AI218708
- F-HEM BB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289
- F-HEM BB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414
- F-HEM BB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
- 20 F-HEM BB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
- F-HEM BB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713
- F-HEM BB1001635//ESTs//0.92:282:60//Hs.126980:AA934077
- F-HEM BB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172
- F-HEM BB1001641//EST//0.11:53:81//Hs.112445:AA594279
- 25 F-HEM BB1001653//EST//0.91:124:64//Hs.144213:T40480
- F-HEM BB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407
- F-HEM BB1001668//ESTs//0.94:83:69//Hs.146202:AI252519
- F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546
- 30 F-HEM BB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496
- F-HEM BB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430
- F-HEM BB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664
- F-HEM BB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398
- 35 F-HEM BB1001706
- F-HEM BB1001707//EST//0.091:241:60//Hs.136830:AA769219
- F-HEM BB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064
- F-HEM BB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219
- F-HEM BB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578
- 40 F-HEM BB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244
- F-HEM BB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144
- F-HEM BB1001753//ESTs//0.00013:35:100//Hs.139643:H06263
- F-HEM BB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077
- 45 F-HEM BB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639
- F-HEM BB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976
- F-HEM BB1001785//EST//0.16:262:60//Hs.162526:AA584102
- F-HEM BB1001797//ESTs//0.37:201:63//Hs.91559:AA806370
- 50 F-HEM BB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951
- F-HEM BB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956
- F-HEM BB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
- F-HEM BB1001831//Homo sapiens PAM COOH terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.0e-13:486:111:100//Hs.136830:AA769219
- F-HEM BB1001834//TRIM11 mRNA, complete cds//1.5e-48:60:100//Hs.81279:U07664
- F-HEM BB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067
- F-HEM BB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

- F-HEM BB1001850//EST//0.0035:204:61//Hs.7311:T23858  
 F-HEM BB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs.155464:AF088219  
 F-HEM BB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752  
 F-HEM BB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371  
 5 F-HEM BB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503  
 F-HEM BB1001872  
 F-HEM BB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478  
 F-HEM BB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.100555:X98743  
 10 F-HEM BB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868  
 F-HEM BB1001899//ESTs//0.17:242:62//Hs.136969:AA830918  
 F-HEM BB1001905  
 F-HEM BB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155  
 F-HEM BB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742  
 15 F-HEM BB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955  
 F-HEM BB1001911  
 F-HEM BB1001915//ESTs//0.92:136:71//Hs.144465:R68882  
 F-HEM BB1001921//EST//2.0e-19:398:67//Hs.44789:N36113  
 20 F-HEM BB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245  
 F-HEM BB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398  
 F-HEM BB1001930//EST//0.043:157:63//Hs.161927:AA483904  
 F-HEM BB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087  
 F-HEM BB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875  
 25 F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390  
 F-HEM BB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669  
 F-HEM BB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101  
 F-HEM BB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070  
 F-HEM BB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418  
 30 F-HEM BB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053  
 F-HEM BB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969  
 F-HEM BB1001973//Myelin oligodendrocyte glycoprotein {alternative products}//2.1e-48:426:78//Hs.53217:Z48051  
 35 F-HEM BB1001983  
 F-HEM BB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051  
 F-HEM BB1001990//ESTs//0.25:171:64//Hs.7961:AA401205  
 F-HEM BB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103  
 F-HEM BB1001997//EST//5.3e-33:294:76//Hs.161041:H82636  
 40 F-HEM BB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964  
 F-HEM BB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093  
 F-HEM BB1002009//ESTs//0.066:441:58//Hs.125313:AI201685  
 F-HEM BB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951  
 F-HEM BB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699  
 45 F-HEM BB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553  
 F-HEM BB1002044  
 F-HEM BB1002045  
 F-HEM BB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256  
 F-HEM BB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661  
 50 F-HEM BB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512  
 F-HEM BB1002069  
 F-HEM BB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239  
 F-HEM BB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625  
 F-HEM BB1002134//ESTs//1.0e-69:398:91//Hs.157492:AI36110  
 F-HEM BB1002139//ESTs//0.64:145:71//Hs.157821:AI362013  
 F-HEM BB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

- F-HEM BB1001850//EST//0.0035:204:61//Hs.7311:T23858  
 F-HEM BB1001863//Small inducible cytokine A5 (RANTES)/3.0e-48:357:82//Hs.155464:AF088219  
 F-HEM BB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752  
 F-HEM BB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371  
 5 F-HEM BB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503  
 F-HEM BB1001872  
 F-HEM BB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478  
 F-HEM BB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.100555:X98743  
 10 F-HEM BB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868  
 F-HEM BB1001899//ESTs//0.17:242:62//Hs.136969:AA830918  
 F-HEM BB1001905  
 F-HEM BB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155  
 F-HEM BB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742  
 15 F-HEM BB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955  
 F-HEM BB1001911  
 F-HEM BB1001915//ESTs//0.92:136:71//Hs.144465:R68882  
 F-HEM BB1001921//EST//2.0e-19:398:67//Hs.44789:N36113  
 20 F-HEM BB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245  
 F-HEM BB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398  
 F-HEM BB1001930//EST//0.043:157:63//Hs.161927:AA483904  
 F-HEM BB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087  
 F-HEM BB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875  
 25 F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390  
 F-HEM BB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669  
 F-HEM BB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101  
 F-HEM BB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070  
 F-HEM BB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418  
 30 F-HEM BB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053  
 F-HEM BB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969  
 F-HEM BB1001973//Myelin oligodendrocyte glycoprotein {alternative products}//2.1e-48:426:78//Hs.53217:Z48051  
 35 F-HEM BB1001983  
 F-HEM BB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051  
 F-HEM BB1001990//ESTs//0.25:171:64//Hs.7961:AA401205  
 F-HEM BB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103  
 F-HEM BB1001997//EST//5.3e-33:294:76//Hs.161041:H82636  
 40 F-HEM BB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964  
 F-HEM BB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093  
 F-HEM BB1002009//ESTs//0.066:441:58//Hs.125313:AI201685  
 F-HEM BB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951  
 F-HEM BB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699  
 45 F-HEM BB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553  
 F-HEM BB1002044  
 F-HEM BB1002045  
 F-HEM BB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256  
 F-HEM BB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661  
 50 F-HEM BB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512  
 F-HEM BB1002069  
 F-HEM BB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239  
 F-HEM BB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625  
 F-HEM BB1002104//ESTs//0.0004:398:91//Hs.157492:AI362013  
 F-HEM BB1002139//ESTs//0.64:145:71//Hs.157821:AI362013  
 F-HEM BB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

F-HEM BB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254

F-HEM BB1002189//EST//0.26:81:70//Hs.147726:AI220208

F-HEM BB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350

F-HEM BB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934

F-HEM BB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332

F-HEM BB1002218//EST//0.015:241:61//Hs.105298:AA489813

F-HEM BB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219

F-HEM BB1002247

F-HEM BB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//

6.8e-47:418:77//Hs.125231:AF068006

F-HEM BB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:AB011166

F-HEM BB1002255//ESTs//0.017:255:61//Hs.126786:U74314

F-HEM BB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//Hs.58169:AF017790

F-HEM BB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998

F-HEM BB1002300

F-HEM BB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.46468:U45984

F-HEM BB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083

F-HEM BB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054

F-HEM BB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188

F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:AJ010841

F-HEM BB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991

F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:U00943

F-HEM BB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838

F-HEM BB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796

F-HEM BB1002381

F-HEM BB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566

F-HEM BB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784

F-HEM BB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456

F-HEM BB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.159897:AB007970

F-HEM BB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150

F-HEM BB1002442

F-HEM BB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087

F-HEM BB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101

F-HEM BB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274

F-HEM BB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885

F-HEM BB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//Hs.74304:AF001691

F-HEM BB1002492//EST//0.24:149:62//Hs.146790:AI149051

F-HEM BB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:M89796

F-HEM BB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494

F-HEM BB1002509//ESTs//0.017:220:63//Hs.155263:AI273725

F-HEM BB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354

F-HEM BB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503

F-HEM BB1002522//EST//0.010:172:62//Hs.147224:AI205719

F-HEM BB1002531

F-HEM BB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219

F-HEM BB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102

F-HEM BB1002556//ESTs//1.0e-10:103:63//Hs.146173:AA906111

F-HEM BB1002558//ESTs//1.0e-10:103:63//Hs.146173:AA906111

F-HEM BB1002579//EST//1.0e-10:103:63//Hs.147935:AI250286

F-HEM BB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

F-HEM BB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254

F-HEM BB1002189//EST//0.26:81:70//Hs.147726:AI220208

F-HEM BB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350

F-HEM BB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934

F-HEM BB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332

F-HEM BB1002218//EST//0.015:241:61//Hs.105298:AA489813

F-HEM BB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219

F-HEM BB1002247

F-HEM BB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//

6.8e-47:418:77//Hs.125231:AF068006

F-HEM BB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:AB011166

F-HEM BB1002255//ESTs//0.017:255:61//Hs.126786:U74314

F-HEM BB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//

Hs.58169:AF017790

F-HEM BB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998

F-HEM BB1002300

F-HEM BB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.46468:U45984

F-HEM BB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083

F-HEM BB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054

F-HEM BB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188

F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:AJ010841

F-HEM BB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991

F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:U00943

F-HEM BB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838

F-HEM BB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796

F-HEM BB1002381

F-HEM BB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566

F-HEM BB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784

F-HEM BB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456

F-HEM BB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.159897:AB007970

F-HEM BB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150

F-HEM BB1002442

F-HEM BB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087

F-HEM BB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101

F-HEM BB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274

F-HEM BB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885

F-HEM BB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//Hs.74304:AF001691

F-HEM BB1002492//EST//0.24:149:62//Hs.146790:AI149051

F-HEM BB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:M89796

F-HEM BB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494

F-HEM BB1002509//ESTs//0.017:220:63//Hs.155263:AI273725

F-HEM BB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354

F-HEM BB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503

F-HEM BB1002522//EST//0.010:172:62//Hs.147224:AI205719

F-HEM BB1002531

F-HEM BB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219

F-HEM BB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102

F-HEM BB1002556//ESTs//1.28e-19:114:61//Hs.146173:AA906111

F-HEM BB1002579//EST//1.0:77:68//Hs.147935:AI250286

F-HEM BB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

- F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657  
 F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:AF089749
- 5 F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817  
 F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945  
 F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058  
 F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323  
 F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
- 10 F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901  
 F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127  
 F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217  
 F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620  
 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811
- 15 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680  
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679  
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124  
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674  
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
- 20 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992  
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614  
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588  
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [*Saccharomyces cerevisiae*]//0.0048:84:83//Hs.20814:AI242922
- 25 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729  
 F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000019  
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
- 30 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945  
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739  
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461  
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [*Mus musculus*]//2.7e-18:330:63//Hs.59906:AA001281
- 35 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019  
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840  
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067  
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174
- 40 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705  
 F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792
- 45 F-MAMMA1000117  
 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508  
 F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402  
 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319  
 F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843
- 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924  
 F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050  
 F-MAMMA1000173//Human protein 11 mRNA (DBP) complete cds//1.2e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657  
 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657  
 F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:AF089749  
 5 F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817  
 F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945  
 F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058  
 F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323  
 F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711  
 10 F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901  
 F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127  
 F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217  
 F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620  
 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811  
 15 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680  
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679  
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124  
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674  
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504  
 20 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992  
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614  
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588  
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [*Saccharomyces cerevisiae*]//0.0048:84:83//Hs.20814:AI242922  
 25 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729  
 F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000019  
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750  
 30 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945  
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739  
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461  
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [*Mus musculus*]//2.7e-18:330:63//Hs.59906:AA001281  
 35 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019  
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840  
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067  
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174  
 40 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705  
 F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792  
 45 F-MAMMA1000117  
 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508  
 F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402  
 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319  
 F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843  
 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924  
 F-MAMMA1000163//ESTs//1.2e-12:104:70//Hs.19559:AA411465  
 F-MAMMA1000165//ESTs//1.0:104:68//Hs.141161:AA029051  
 F-MAMMA1000170//Human drebrin L2 mRNA (DBNL2), complete cds//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657  
 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

- F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739  
 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035  
 F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926  
 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913  
 5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873  
 F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587  
 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543  
 F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015  
 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874  
 10 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087  
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726  
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361  
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505  
 F-MAMMA1000284  
 15 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087  
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641  
 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243  
 F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529  
 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519  
 20 F-MAMMA1000313  
 F-MAMMA1000331  
 F-MAMMA1000339  
 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC  
 REGION [*Saccharomyces cerevisiae*]//2.9e-11:87:93//Hs.13096:AA180963  
 25 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892  
 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.  
 158095:AB007953  
 F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503  
 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087  
 30 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569  
 F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:  
 98//Hs.32170:AB015132  
 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590  
 35 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503  
 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:  
 117:84//Hs.83916:U53468  
 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725  
 F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092  
 40 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME  
 III [*C.elegans*]//9.8e-33:267:81//Hs.32370:AA521111  
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532  
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:  
 AF061573  
 45 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459  
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:  
 AF034546  
 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830  
 50 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:  
 AB011166  
 F-MAMMA1000446  
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [*C.elegans*]//5.1e-08:58:  
 93//Hs.9043:W21827  
 F-MAMMA1000460//EST//0.58:111:63//Hs.56711:U49811  
 F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830  
 F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

- F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739  
 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035  
 F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926  
 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913  
 5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873  
 F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587  
 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543  
 F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015  
 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874  
 10 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087  
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726  
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361  
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505  
 F-MAMMA1000284  
 15 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087  
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641  
 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243  
 F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529  
 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519  
 20 F-MAMMA1000313  
 F-MAMMA1000331  
 F-MAMMA1000339  
 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963  
 25 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892  
 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.  
 158095:AB007953  
 F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503  
 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087  
 30 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569  
 F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:  
 98//Hs.32170:AB015132  
 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590  
 35 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503  
 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:  
 117:84//Hs.83916:U53468  
 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725  
 F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092  
 40 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME  
 III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111  
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532  
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:  
 AF061573  
 45 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459  
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:  
 AF034546  
 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830  
 50 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:  
 AB011166  
 F-MAMMA1000446  
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:  
 93//Hs.9043:W21827  
 F-MAMMA1000459//EST//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000460//EST//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830  
 F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

- F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830  
 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948  
 F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482  
 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219  
 5 F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878  
 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352  
 F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497  
 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352  
 F-MAMMA1000565  
 10 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete  
 cds//5.8e-51:404:80//Hs.125231:AF068006  
 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045  
 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780  
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete  
 15 cds//8.8e-45:390:78//Hs.159523:AF001622  
 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744  
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886  
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519  
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494  
 20 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478  
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605  
 F-MAMMA1000623  
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751  
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:  
 25 AF023674  
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353  
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107:  
 K00629  
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490  
 30 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743  
 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:  
 U13220  
 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627  
 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081  
 35 F-MAMMA1000713//Acetylcholinesterase [I4-E5 domain] [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//  
 Hs.157124:S71129  
 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275  
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648  
 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247  
 40 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:  
 AA700024  
 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513  
 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.  
 158095:AB007953  
 45 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075  
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:  
 AF100141  
 F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580  
 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:  
 50 AB011147  
 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494  
 F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663  
 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217:  
 Z18051  
 F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288  
 F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

- F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830  
 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948  
 F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482  
 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219  
 5 F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878  
 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352  
 F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497  
 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352  
 F-MAMMA1000565  
 10 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete  
 cds//5.8e-51:404:80//Hs.125231:AF068006  
 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045  
 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780  
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete  
 15 cds//8.8e-45:390:78//Hs.159523:AF001622  
 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744  
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886  
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519  
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494  
 20 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478  
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605  
 F-MAMMA1000623  
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751  
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:  
 25 AF023674  
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353  
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107:  
 K00629  
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490  
 30 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743  
 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:  
 U13220  
 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627  
 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081  
 35 F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//  
 Hs.157124:S71129  
 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275  
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648  
 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247  
 40 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:  
 AA700024  
 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513  
 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.  
 158095:AB007953  
 45 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075  
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:  
 AF100141  
 F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580  
 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:  
 50 ABO11147  
 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494  
 F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663  
 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217:  
 748051  
 F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288  
 F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

- F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114  
 F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137  
 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575  
 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849  
 5 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130  
 F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089  
 F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219  
 F-MAMMA1000841  
 F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//  
 10 Hs.82210:U47742  
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696  
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877  
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022  
 F-MAMMA1000855  
 15 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906  
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135  
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342  
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172  
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812  
 20 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777  
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459  
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147  
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:  
 484:94//Hs.138938:AA012894  
 25 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812  
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465  
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:  
 X67055  
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683  
 30 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506  
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081  
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628  
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239  
 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.  
 35 116007:S79267  
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968  
 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid  
 dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785  
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734  
 40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303  
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714  
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474  
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//  
 Hs.129735:AF010144  
 45 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814  
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096  
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802  
 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062  
 F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007  
 50 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724  
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711  
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:  
 Y15718  
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:B93968  
 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857  
 F-MAMMA1001038

F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114  
 F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137  
 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575  
 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849  
 5 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130  
 F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089  
 F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219  
 F-MAMMA1000841  
 F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//  
 10 Hs.82210:U47742  
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696  
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877  
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022  
 F-MAMMA1000855  
 15 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906  
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135  
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342  
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172  
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812  
 20 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777  
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459  
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147  
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.4e-91:  
 484:94//Hs.138938:AA012894  
 25 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812  
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465  
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:  
 X67055  
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683  
 30 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506  
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081  
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628  
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239  
 F-MAMMA1000931//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]/1.0e-25:312:66//Hs.  
 35 116007:S79267  
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968  
 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid  
 dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785  
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734  
 40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303  
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714  
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474  
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//  
 Hs.129735:AF010144  
 45 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814  
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096  
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802  
 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062  
 F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007  
 50 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724  
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711  
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:  
 Y15718  
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968  
 F-MAMMA1001035//ESTs//6.4e-28:268:77//Hs.139536:AA180857  
 F-MAMMA1001038

- F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178  
 F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882  
 F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719
- 5 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503  
 F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585  
 F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116  
 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749
- 10 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503  
 F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420  
 F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896  
 F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254
- 15 F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627  
 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045  
 F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915
- 20 F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219  
 F-MAMMA1001133  
 F-MAMMA1001139  
 F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534  
 F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217
- 25 F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741  
 F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147  
 F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299  
 F-MAMMA1001181
- 30 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171  
 F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083  
 F-MAMMA1001198  
 F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
- 35 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974  
 F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776  
 F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200  
 F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087
- 40 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534  
 F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587  
 F-MAMMA1001244  
 F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476
- 45 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121  
 F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149  
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561  
 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503
- 50 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747  
 F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522  
 F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832  
 F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998  
 F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426  
 F-MAMMA1001297//ESTs//1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM/2.7e-10:357:65//Hs.119000:M95178  
F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882  
F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog/7.9e-87:415:99//Hs.135623:AA134719  
F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503  
F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585  
F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116  
F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749  
F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503  
F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420  
F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896  
F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254  
F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627  
F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045  
F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915  
F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219  
F-MAMMA1001133  
F-MAMMA1001133  
F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534  
F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217  
F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741  
F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147  
F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299  
F-MAMMA1001181  
F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171  
F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083  
F-MAMMA1001198  
F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348  
F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974  
F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/5.5e-25:275:75//Hs.105292:AA504776  
F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200  
F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087  
F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534  
F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587  
F-MAMMA1001244  
F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476  
F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121  
F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149  
F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561  
F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503  
F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747  
F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522  
F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832  
F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998  
F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757106  
F-MAMMA1001305//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503  
F-MAMMA1001305//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503  
GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat  
1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087  
 F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147  
 F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806  
 F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197  
 5 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267  
 F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258  
 F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981  
 F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR//4.6e-09:415:58//Hs.839:M86826  
 10 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402  
 F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763  
 F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928  
 F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394  
 F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.  
 15 46328:D87942  
 F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:71//Hs.37181:D64108  
 F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321  
 F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590  
 F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040  
 20 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053  
 F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:72//Hs.75939:  
 D78335  
 F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874:  
 AA524909  
 25 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366  
 F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269  
 F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795  
 F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506  
 F-MAMMA1001547  
 30 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:  
 AB007931  
 F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866:  
 AI017072  
 F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764  
 35 F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339  
 F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132  
 F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375  
 F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266  
 F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152  
 40 F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727  
 F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc  
 Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-  
 67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger  
 protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and  
 45 DXS1055//1.4e-40:447:73//Hs.154353:AL022165  
 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796  
 F-MAMMA1001635  
 F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524  
 F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:  
 50 68//Hs.59829:AB014602  
 F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:  
 AB007917  
 F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:  
 AI027548  
 F-MAMMA1001686//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:  
 AI027548  
 F-MAMMA1001687//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:  
 AI027548  
 F-MAMMA1001688//ESTs//1.6e-92:480:96//Hs.118496:AA036889  
 F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:327.81//Hs.138404:R70986

F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870

F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497

F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905

F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242

F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487

F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552

F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300

F-PLACE1005898

F-PLACE1005921

F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504

F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274

F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:M18391

F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142

F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978

F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357

F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468

F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:AI357868

F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:U13948

F-PLACE1005968

F-PLACE1005990

F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981

F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256

F-PLACE1006011

F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743

F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:AB018332

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906

F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395

F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:AF039023

F-PLACE1006129

F-PLACE1006139

F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353

F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]//2.9e-12:119:84//Hs.23153:R92857

F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868

F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239

F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005

F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433

F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608

F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719

F-PLACE1006205

F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:AI279486

F-PLACE1006225

F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668

F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185

F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802

F-PLACE1006248

F-PLACE1006249

F-PLACE1006250

F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625

F-PLACE1006318

F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503

F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492

F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249

F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481

F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581

F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715

F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693

F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085

F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129

F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866

F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470

F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194

F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511

F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493

F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584

F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542

F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358

F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219

F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784

F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529

F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280

F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670

F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088

F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858

F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396

F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473

F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917

F-PLACE1006678

F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403

F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612

F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354

F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152

F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252

F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783

F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228

F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.123642:M83941

F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017

F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892

F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518

F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:87//Hs.23094:M10500

F-PLACE1006829//ESTs//1.5e-21:111:94//Hs.12988:AA11481

F-PLACE1006860//ESTs//1.0e-206:206:65//Hs.158793:AI376777

F-PLACE1006867//ESTs//1.0e-218:62//Hs.91106:AA551270

F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254

- F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601  
 F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187  
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443  
 F-PLACE1006917  
 5 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913  
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211  
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565  
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723  
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [*Saccharomyces cerevisiae*]//3.2e-07:67:98//Hs.  
 10 21806:AA630312  
 F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417  
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:  
 191:67//Hs.8813:AF032922  
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753  
 15 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//  
 3.1e-05:594:58//Hs.32951:AF034102  
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971  
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503  
 F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957  
 20 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243  
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987  
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-  
 gen storage disease type iii)//0.18:268:63//Hs.904:U84010  
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385  
 25 F-PLACE1007112  
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121  
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601  
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965  
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669  
 30 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204  
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//  
 Hs.80598:D50495  
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141  
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467  
 35 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909  
 F-PLACE1007274  
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:  
 L06133  
 F-PLACE1007282  
 40 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436  
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412  
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//  
 Hs.144877:AF029403  
 F-PLACE1007342  
 45 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:  
 567:98//Hs.76596:AF096870  
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173  
 F-PLACE1007375  
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642  
 50 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287  
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//  
 Hs.14387:AF093771  
 F-PLACE1007416  
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436  
 55 F-PLACE1007452//EST//1.3e-34:121:64//Hs.151708:AA554714  
 F-PLACE1007460//ESTs//1.0e-42:440:74//Hs.141722:AA769103

F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975

F-PLACE1007488

F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385

F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503

F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296

F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979

F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080

F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755

F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:AB014561

F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863

F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257

F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163

F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533

F-PLACE1007621

F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867

F-PLACE1007645

F-PLACE1007649

F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266

F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055

F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503

F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812

F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953

F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:AF061243

F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:AA476815

F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:64//Hs.104129:AA923278

F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:AB014585

F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424

F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030

F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469

F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656

F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504

F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107

F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841

F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635

F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503

F-PLACE1007852

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:AB018309

F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387

F-PLACE1007877

F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.92381:AB007956

F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002

F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.5671:AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:730:98//Hs.78106:AF079529

F-PLACE1007969//ESTs//1.1e-10:100:100//Hs.100000:AA000000

F-PLACE1007970

F-PLACE1007971//ESTs//1.1e-10:100:100//Hs.100000:AA000000

F-PLACE1008000//Homo sapiens vein 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031

F-PLACE1008044

F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382

F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060

F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:U60975

F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197

F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769

F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874

F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683

F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]/5.1e-20:124:95//Hs.146238:AI263135

F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427

F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524

F-PLACE1008201

F-PLACE1008209

F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856

F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385

F-PLACE1008273

F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113

F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970

F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287

F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071

F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129

F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]/5.4e-74:356:98//Hs.105382:AA496362

F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579

F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569

F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911

F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171

F-PLACE1008398

F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326

F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943

F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653

F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499

F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]/0.019:530:58//Hs.72248:S72487

F-PLACE1008437

F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335

F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901

F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381

F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:U10886

F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823

F-PLACE1008524

F-PLACE1008532//Thromboxane A<sub>2</sub> receptor-like receptor mRNA, complete cds//1.0:304:60//Hs.24040:AF006823

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997

F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069

F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:AB018334

F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087:AA649326

F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794

F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560

F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458

F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211

F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394

F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535

F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333

F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728

F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406

F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741

F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080

F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503

F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:AF060543

F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772

F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542

F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905

F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883

F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858

F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728

F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563

F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503

F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308

F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771

F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026

F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937

F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308

F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950

F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112

F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762

F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689

F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585

F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698

F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525

F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800

F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091

F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031

F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011

F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890

F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788

F-PLACE1009113//ESTs//1.1e-11:111:63//Hs.160997:H55762

F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215

F-PLACE1009150//Human HSLIM15 mRNA for HsLim15, complete cds//1.7e-50:440:78//Hs.37181:D64108

F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.158095:AB007953

F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614:M62302

F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250

F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770

F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821

F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100

F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396

F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689

F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131

F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540

F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575

F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735

F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192

F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503

F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767

F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473

F-PLACE1009368

F-PLACE1009375

F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394

F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878

F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863

F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262

F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630

F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872

F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680

F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.00039:347:60//Hs.994:M95678

F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67AI//4.1e-91:464:96//Hs.155049:AC004531

F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839

F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405

F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728

F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417

F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956

F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866

F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291

F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806

F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394

F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011

F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085

F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773

F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087

F-PLACE1009639

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159

F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494

F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL PROTEIN REPEATS CONTAINING REPEATS OF A 14-PHASE INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926

F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789

F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024

F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989

F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996

F-PLACE1009845

F-PLACE1009861

F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021

F-PLACE1009886

F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889

F-PLACE1009908

F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717

F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379

F-PLACE1009925

F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153

F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446

F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345

F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114

F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540

F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529

F-PLACE1010023

F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878

F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.142151:AA984061

F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482

F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925

F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus]//1.8e-38:212:95//Hs.98067:AA236822

F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:U69567

F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569

F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682

F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889

F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740

F-PLACE1010152

F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792

F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582

F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:H69637

F-PLACE1010231

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917

F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590

F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540

F-PLACE1010275//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540

F-PLACE1010280//HOMEOBOX PROTEIN DOMAIN PROTEIN RD1//1.5e-62:44:82//Hs.4096:U1143

F-PLACE1010321//Human nSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248

F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659

F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117

F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855

F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648

F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986

F-PLACE1010401

F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:U70824

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:AF039081

F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500

F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100

F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:64//Hs.159273:AF054177

F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472

F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979

F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148

F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186

F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394

F-PI ACF1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60656

F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778

F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200

F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461

F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225

F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102

F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076

F-PLACE1010662

F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376

F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027

F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564

F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244

F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391

F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284

F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140

F-PLACE1010786

F-PLACE1010800

F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157

F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085

F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.132736:AA583494

F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048

F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs.130135:AA905493

F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244

F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182

F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671

F-PLACE1010900

F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981

F-PLACE1010917

F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537  
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:  
 AB011126  
 5 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:  
 AF064244  
 F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985  
 F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154  
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59//Hs.585:X04506  
 F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632  
 10 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721  
 F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931  
 F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032  
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:  
 U10886  
 15 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-  
 11:207:68//Hs.994:M95678  
 F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:78//Hs.2407:Z49194  
 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//  
 Hs.153640:U56998  
 20 F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320  
 F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663  
 F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037  
 F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317  
 F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857  
 25 F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949  
 F-PLACE1011160  
 F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443  
 F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-  
 124:576:99//Hs.159140:AF038664  
 30 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469:99//Hs.8241:AA283057  
 F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:221:  
 88//Hs.101821:W27452  
 F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751  
 35 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:99//Hs.23168:  
 AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:98//Hs.15144:AC005014  
 F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803  
 F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:  
 40 AF070637  
 F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915  
 F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160  
 F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310  
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:  
 45 99//Hs.5819:AF102265  
 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.  
 159897:AB007970  
 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535  
 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325:99//  
 50 Hs.107245:AA627053  
 F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868  
 F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552  
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:  
 AB011102

F-PLACE1011433

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:

AB011102  
 F-PLACE1011433//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138  
 AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482

F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264

F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997

5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319

F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476

F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333

F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180

10 F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462

F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778

F-PLACE1011641

F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631

15 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661

F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086

F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745

F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234

20 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366

F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350

F-PLACE1011725

F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853

F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891

25 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240

F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693

F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660

F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664

F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775

30 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152

F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913

F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868

F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817

35 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617

F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763

F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514

F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591

F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514

40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256

F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956

F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503

45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330

F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627

F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831

F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627

F-PLACE2000017

50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557

F-PLACE2000030

F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512

F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.93664:N23366

F-PLACE2000035//EST//0.00014:213:64//Hs.119889:AA705319

F-PLACE2000047//ESTs//4.4e-32:328:75//Hs.141024:AI285997

F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966

F-PLACE2000061

F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457  
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219  
 F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333  
 5 F-PLACE2000100  
 F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219  
 F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:U56417  
 F-PLACE2000115  
 10 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353  
 F-PLACE2000132  
 F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:AA718911  
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645  
 15 F-PLACE2000164  
 F-PLACE2000170  
 F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179  
 F-PLACE2000176  
 F-PLACE2000187  
 20 F-PLACE2000216  
 F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933  
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296  
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338  
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958  
 25 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522  
 F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560  
 F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869  
 F-PLACE2000317  
 30 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796  
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088  
 F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299  
 F-PLACE2000347//ESTs, Moderately similar to F18547\_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817  
 35 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645  
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045  
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861  
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032  
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638  
 40 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953  
 F-PLACE2000398  
 F-PLACE2000399  
 F-PLACE2000404  
 45 F-PLACE2000411  
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080  
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966  
 F-PLACE2000427  
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719  
 50 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257  
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019  
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080  
 F-PLACE2000455//ESTs, Moderately similar to "" ALU SUBFAMILY SC WARNING ENTRY "" [H.sapiens]//4.0e-10:100:100//Hs.113283:AF018080  
 F-PLACE2000458//H.sapiens mRNA for protein ""//1.0e-54:51:11//Hs.113283:AF018080  
 F-PLACE2000465//ESTs//4.4e-36:377:75//Hs.55855:AA621381  
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,  
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384  
 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128

F-PLACE3000029

F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248

F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842

F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.122752:AF026445

F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295

F-PLACE3000121

F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081

F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603

F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243

F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016

F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871

F-PLACE3000148

F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572

F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023

F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666

F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147

F-PLACE3000160

F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219

F-PLACE3000194

F-PLACE3000197

F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546

F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975

F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744

F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216

F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377

F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019

F-PLACE3000226

F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046

F-PLACE3000244

F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858

F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650

F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944

F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770

F-PLACE3000310

F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586

F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219

F-PLACE3000331

F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545

F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741

F-PLACE3000350//ESTs. Highly similar to SERINE/THREONINE-PROTEIN KINASE SUII HICapochabdic acid  
 F-PLACE3000352//H. sapiens cDNA for octamer binding factor 1, 4848-4878 bp, 1407-2440 bp

F-PLACE3000353//H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78

234.63//Hs.7498:U41514

F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441

F-PLACE3000363

F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928

F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641

5 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432

F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637

F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785

F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270

F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715

10 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541

F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263

F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:H61502

15 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:AB018344

F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161

F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202

20 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874

F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888

F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:AB018352

25 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:AC004131

F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533

F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.40993:AF000148

30 F-PLACE4000063

F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713

F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819

F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058

35 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931

F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751

F-PLACE4000129

F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627

F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856

40 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367

F-PLACE4000192

F-PLACE4000211

F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594

F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329

45 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317

F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250

F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609

F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886

50 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200

F-PLACE4000261

F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

F-PLACE4000270

F-PLACE4000271

F-PLACE4000320//Homo sapiens mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329

F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365

F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292

F-PLACE4000367

F-PLACE4000369

F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256

F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823

F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:AB014540

F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982

F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200

F-PLACE4000445

F-PLACE4000450

F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874

F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075

F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951

F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289

F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731

F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022

F-PLACE4000548

F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:AF000986

F-PLACE4000581

F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080

F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675

F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074

F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:AB002446

F-PLACE4000650

F-PLACE4000654

F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132

F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299

F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299:AB014554

F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254

F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877

F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313

F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194

F-THYRO1000034

F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099

F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326

F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345

F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557

F-THYRO1000085

F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065

F-THYRO1000107

F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:86//Hs.23094:M19503

F-THYRO1000121

F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U70732

F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:AF087142

F-THYRO1000155//EST//1.1e-58:158:58//Hs.139634:AA478411

F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219

F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

152936:D63475

F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

5 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590

F-THYRO1000270

15 F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068

F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803

F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175

20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:64//Hs.7833:U29091

F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919

25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB011134

F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855

F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413

30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572

F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238

F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773

F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520

35 F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663

F-THYRO1000488

F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298

F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120

40 F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949

45 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081

50 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125

F-THYRO1000658//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267

F-THYRO1000662

F-THYRO1000665

F-THYRO1000676//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380

F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452  
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324  
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204  
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085  
 5 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871  
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:AF061573  
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481  
 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084  
 10 F-THYRO1000787  
 F-THYRO1000793  
 F-THYRO1000796  
 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:AB002446  
 15 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087  
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339  
 F-THYRO1000843  
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788  
 20 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170  
 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103  
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531  
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.92381:AB007956  
 25 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529  
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836  
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263  
 30 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963  
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169  
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907  
 F-THYRO1000983  
 35 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646  
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307  
 F-THYRO1001003  
 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369  
 F-THYRO1001033//H.sapiens mRNA for cyclin I//0.0061:287:60//Hs.3232:Z46788  
 40 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830  
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353  
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130  
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700  
 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416  
 45 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425  
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074  
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788  
 F-THYRO1001173  
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385  
 50 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163  
 F-THYRO1001204  
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219  
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461  
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:U53204  
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836  
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872  
 F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333  
 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545  
 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207  
 5 F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939  
 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877  
 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:AB014607  
 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993  
 10 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946  
 F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694  
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659  
 F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788  
 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//  
 15 Hs.102877:U41315  
 F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099  
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215  
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830  
 F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943  
 20 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904  
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663  
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211  
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046  
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335  
 25 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572  
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655  
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535  
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849  
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071  
 30 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046  
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659  
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:M91463  
 F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568  
 35 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089  
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238  
 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552  
 F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691  
 40 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//Hs.3826:U69560  
 F-THYRO1001738//EST//6.9e-30:180:94//Hs.58641:W81229  
 F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813  
 F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590  
 45 F-THYRO1001772//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725  
 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324  
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295  
 F-THYRO1001828  
 50 F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823  
 F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.51061:M24283  
 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198  
 F-VESEN1000122  
 F-THYRO1000037//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305

U78521

F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//  
0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.  
9242:AF081192

F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623

F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

F-Y79AA1000328

F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:  
AF071309

F-Y79AA1000346

F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219

F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018

F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:  
AF082516

F-Y79AA1000480

F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871

F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521

F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356

F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:  
AF068706

F-Y79AA1000574//Human mRNA for GC box binding protein, complete cds//0.95:258:62//Hs.150557:D31716

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:  
AF091080F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:  
AF060503

F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513

F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:  
98//Hs.83023:AF093670

F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969

F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377

F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067

F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:  
AF098799

F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:  
AF059569

F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//  
0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA 4 CHAIN//6.9e-107:603:90//Hs.75218:X26956

F-Y79AA1000848//Homo sapiens alpha 2-macroglobulin receptor type 1 mRNA, complete cds//1.1e-107:107:107//Hs.1016815

F-Y79AA1000848//Homo sapiens alpha 2-macroglobulin receptor type 1 mRNA, complete cds//1.1e-107:107:107//Hs.1016815

1016815

F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

- F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]/6.9e-69:310:94//Hs.76822:AI359536
- F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
- F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
- 5 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
- F-Y79AA1001023
- F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
- F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
- F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
- 10 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511
- F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
- F-Y79AA1001078
- F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
- 15 F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
- F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
- F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
- F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
- F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
- 20 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
- F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
- F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
- F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
- 25 F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
- F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
- F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
- F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
- F-Y79AA1001384
- 30 F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
- F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]/1.5e-90:424:96//Hs.154221:H23167
- F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489
- F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
- F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
- 35 F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]/0.95:256:63//Hs.29974:AI360447
- F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
- F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
- F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
- 40 F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
- F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
- F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
- F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
- F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583
- 45 F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]/9.4e-79:421:94//Hs.107039:W27244
- F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
- F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526
- 50 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
- F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
- F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
- F-Y79AA1001711//ESTs//5.0e-29:504:82//Hs.100461:AI018600
- F-Y79AA1001805//ESTs//1.0e-102:179:98//Hs.100461:AI018600
- F-Y79AA1001827//ESTs, Weakly similar to Similar to S cerevisiae YD9335.03c protein [H. sapiens]/2.9e-62:310:98//Hs.15709:W81213

- F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533  
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124  
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332  
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778  
 5 F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173  
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720  
 F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382  
 F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611  
 10 F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943  
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:AI338045  
 F-Y79AA1002093  
 F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865  
 F-Y79AA1002115  
 15 F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395  
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955  
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538  
 F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515  
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotenax]//2.3e-113:568:  
 20 96//Hs.111637:AA305890  
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984  
 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477  
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508  
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045  
 25 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:  
 AB014592  
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:  
 AB014555  
 30 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:  
 AB014534  
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999  
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete  
 35 cds//0.028:587:58//Hs.2363:L36069  
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377  
 F-Y79AA1002399  
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569  
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142  
 40 F-Y79AA1002431  
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318  
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973  
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765  
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302  
 45

## Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by "

[0312] The data are not shown for the clones in which the P-value was higher than 1

[0313] The data are not shown for the clones in which the P-value was higher than 1

R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]/5.6e-93:501:93//Hs.13015:AA628434

R-HEMBA1000030//Human POU domain protein (Bm-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233

R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198

R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087

R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340

R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329

R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788

R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]/4.4e-90:502:90//Hs.55918:AA151667

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:AB018340

R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:AB014540

R-nnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]/7.7e-92:428:100//Hs.126925:AA931237

R-HEMBA1000158

R-nnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]/1.3e-05:58:91//Hs.5570:AI377863

R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545

R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366

R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927

R-HEMBA1000201//Human Inl1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847

R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311

R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532

R-nnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404

R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874

R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:AB007944

R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019

R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808

R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424

R-nnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]/4.9e-14:208:73//Hs.93332:AA811920

R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485

R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962

R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409

R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099

R-nnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323

R-nnnnnnnnnnnn//Human Ca<sup>2+</sup>-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//Hs.151301:U36448

R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]/1.1e-103:489:99//Hs.108881:AI018024

R-nnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238

R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560

R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460

R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243

R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629

R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857

R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938

R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960

R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460

R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878

R-HEMBA1000396//EST, Weakly similar to ... protein [R.norvegicus] ...

R-HEMBA1000411//ESTs, Weakly similar to ankyrin-3 long form [H.sapiens]/6.1e-92:373:99//Hs.48675:AI005282

- R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700  
 R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140  
 R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189  
 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143  
 5 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014  
 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349  
 R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316  
 R-HEMBA1000460  
 R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370  
 10 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219  
 R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449  
 R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528  
 R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087  
 15 R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571  
 R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318  
 R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531  
 R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885  
 R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414  
 20 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280  
 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:U15782  
 R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277  
 25 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809  
 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317  
 R-nnnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699  
 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881  
 R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481  
 30 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196  
 R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128  
 R-nnnnnnnnnnnnn  
 R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788  
 35 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944  
 R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509  
 R-HEMBA1000592//TYROSINE-PROTEIN KINASE  
 ITK/TSK//0.024:309:61//Hs.89519:L10717  
 40 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041  
 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136  
 R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424  
 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438  
 45 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235  
 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590  
 R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390  
 50 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929  
 R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136  
 R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922  
 R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000686//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000687//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000688//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000689//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000690//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000691//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000692//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000693//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000694//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000695//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000696//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000697//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000698//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000699//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000700//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000701//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000702//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000703//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000704//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403  
 R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213

R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612

R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:U33931

R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777

R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110

R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219

R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131

R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.10458:AF088219

R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612

R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//1.3e-48:284:90//Hs.103458:X53795

R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087

R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939

R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977

R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258

R-HEMBA1000851

R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:U46689

R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794

R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202

R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608

R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951

R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219

R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154

R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672

R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508

R-HEMBA1000919

R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597

R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619

R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291

R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074

R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750

R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.159187:AB007977

R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498

R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590

R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170

R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878

R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464

R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902

R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881

R-HEMBA1001007

R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764

R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:AB007937

R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-140:35:41:56000:Y05000

R-HEMBA1001022//ESTs//3.4e-100:100:100//Hs.63243:AI120351

R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336

R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

R-nnnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616

R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:AB014521

R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886

R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813

R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420

R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.127338:AB007961

R-HEMBA1001080

R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788

R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674

R-HEMBA1001094

R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245

R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219

R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974

R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320

R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530

R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341

R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265

R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219

R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358

R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:AB007961

R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896

R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194

R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080

R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316

R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932

R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728

R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435

R-nnnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181

R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674

R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534

R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324

R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219

R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162

R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214

R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019

R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977

R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950

R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838

R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259

R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080

R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816

R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837

R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334

R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550

R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458

R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482

R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439

R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204

R-HEMBA1001398//Homo sapiens mRNA for IL-6 receptor/4.0e-46:279:84//Hs.120905:R22204

R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714

R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364

R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199  
 R-HEMBA1001415  
 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981  
 R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704  
 5 R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263  
 R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982  
 R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546  
 R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077  
 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503  
 10 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220  
 R-HEMBA1001463  
 R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008  
 R-HEMBA1001478  
 R-HEMBA1001497  
 15 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426  
 R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503  
 R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269  
 R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493  
 R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723  
 20 R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270  
 R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348  
 R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219  
 R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324  
 R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880  
 25 R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030  
 R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652  
 R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329  
 R-HEMBA1001589  
 R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]/6.9e-71:431:88//Hs.26625:W25874  
 30 R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:K00627  
 R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530  
 R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694  
 35 R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158  
 R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]/1.2e-86:442:95//Hs.63888:AA203398  
 R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554  
 R-HEMBA1001658  
 40 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343  
 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943  
 R-HEMBA1001675  
 45 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962  
 R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424  
 R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916  
 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598  
 50 R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960  
 R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095  
 R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]/1.8e-46:236:98//Hs.132948:AA194452  
 R-HEMBA1001715//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001716//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001717//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001718//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001719//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001720//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001721//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001722//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001723//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001724//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001725//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001726//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001727//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001728//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001729//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001730//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]  
 R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353  
 R-HEMBA1001744  
 R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623  
 R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162  
 5 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145  
 R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306  
 R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721  
 R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053  
 R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243  
 10 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823  
 R-nnnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019  
 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.  
 118164:AB007969  
 R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334  
 15 R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179  
 R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290  
 R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707  
 R-nnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578  
 R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210  
 20 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250  
 R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513  
 R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446  
 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:  
 AB014517  
 25 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853  
 R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative products}//1.9e-37:357:76//Hs.53217:  
 Z48051  
 R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.  
 9489:R84329  
 30 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969  
 R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128  
 R-HEMBA1001910  
 R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:  
 347:100//Hs.30991:AA994438  
 35 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.  
 91251:U66685  
 R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706  
 R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125  
 R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:  
 40 534:96//Hs.154934:AF000145  
 R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-  
 99:482:98//Hs.96849:AA879470  
 R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390  
 R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668  
 45 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452  
 R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866  
 R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421  
 R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048  
 R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825  
 50 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/  
 Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains  
 a putative CpG island. ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178  
 R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932  
 R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717  
 R-HEMBA1001988//ESTs//1.1e-47:292:89//Hs.163333:AA879053  
 R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase, catalytic subunit, isoform 1  
 R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930  
 R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550  
 R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538  
 R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312  
 R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:  
 5 AB011135  
 R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764  
 R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996  
 R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354  
 R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369  
 10 R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402  
 R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:  
 AF065854  
 R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868  
 R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957  
 15 R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734  
 R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199  
 R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642  
 R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337  
 R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:  
 20 AF023674  
 R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915  
 R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043  
 R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081  
 R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457  
 25 R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete  
 cds//6.0e-42:419:73//Hs.159523:AF001622  
 R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:  
 AB007958  
 R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357  
 30 R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503  
 R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342  
 R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315  
 R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151  
 R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:  
 35 AB014606  
 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//  
 Hs.25664:AF089814  
 R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202  
 R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426  
 40 R-HEMBA1002257  
 R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGEN-  
 IC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675  
 R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314  
 R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595  
 45 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818  
 R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679  
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:  
 AB018314  
 R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822  
 50 R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094  
 R-nnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:  
 661:93//Hs.119023:AF092563  
 R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435  
 R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237  
 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen in sapiens, complete cds//1.2e-124:124:124//Hs.119023:AF092563  
 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267  
 R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069  
R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085  
R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395  
R-nnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193  
R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394  
R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219  
R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995  
R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133  
R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449  
R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990  
R-nnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972  
R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715  
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:AB007923  
R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700  
R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804  
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881  
R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012  
R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519  
R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219  
R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:AF075587  
R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904  
R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838  
R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055  
R-HEMBA1002621  
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:AB018351  
R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881  
R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715  
R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041  
R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970  
R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696  
R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307  
R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945  
R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896  
R-nnnnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396  
R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282  
R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477  
R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:AB018315  
R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884  
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521  
R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168  
R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163  
R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526  
R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792  
R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090  
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.1e-40:244:58//Hs.43041:N22112  
R-HEMBA1002771//EST//4.2e-44:58//Hs.43041:N22112  
R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491  
R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717

R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333  
 R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709  
 R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320  
 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:  
 5 AF071185  
 R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204  
 R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013  
 R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.  
 5337:AA243757  
 R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514  
 R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830  
 R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827  
 R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670  
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//  
 15 Hs.33787:AF037261  
 R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011  
 R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820  
 R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087  
 R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481  
 20 R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165  
 R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679  
 R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732  
 R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892  
 R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085  
 25 R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369  
 R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405  
 R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579  
 R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219  
 R-nnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064  
 30 R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:  
 96//Hs.125749:AI377682  
 R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080  
 R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480  
 R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577  
 35 R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827  
 R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366  
 R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN  
 CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442  
 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-  
 40 119:578:97//Hs.44097:AF054182  
 R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627  
 R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238  
 R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903  
 R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235  
 45 R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402  
 R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249  
 R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219  
 R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223  
 R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//  
 50 Hs.104800:AA709155  
 R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624  
 R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058  
 R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.  
 18717:U18675  
 R-HEMBA1003135//ESTs, Weakly similar to MANNULOSE-6-PHOSPHATE 6-EPIMERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615  
 R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670  
 R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933  
 R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389  
 R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000  
 5 R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804  
 R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540  
 R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943  
 R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265  
 10 R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817  
 R-HEMBA1003227//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:W27666  
 R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305  
 15 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834  
 R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864  
 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929  
 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219  
 20 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392  
 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785  
 R-HEMBA1003281  
 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109  
 25 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266  
 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353  
 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504  
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872  
 30 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869  
 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119  
 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173  
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029  
 35 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357  
 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540  
 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651  
 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588  
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247  
 40 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-11:261:65//Hs.87578:AI125363  
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847  
 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127  
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204  
 45 R-HEMBA1003417//ESTs//1.7e-24:188:85//Hs.70266:Z78309  
 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563  
 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013  
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696  
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121  
 50 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516  
 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080  
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688  
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760  
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68  
 R-HEMBA1003545//ESTs//1.1e-42:310:85//Hs.23294:W27666  
 R-HEMBA1003548//ESTs//1.4e-60:74:60//Hs.148336:AA91167  
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.91619:AA552351

R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734  
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522  
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058  
 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.  
 5 58598:AA625440  
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099  
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892  
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065  
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212  
 10 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087  
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042  
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374  
 R-HEMBA1003615  
 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167  
 15 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387  
 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888  
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021  
 R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:  
 189:84//Hs.142208:AA209438  
 20 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830  
 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010  
 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783  
 R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.  
 67619:AB007957  
 25 R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049  
 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635  
 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.  
 9489:R84329  
 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083  
 30 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.  
 22934:AA581379  
 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916  
 R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:  
 M29873  
 35 R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064  
 R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.  
 1139:X77777  
 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080  
 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//1.2e-  
 40 33:377:74//Hs.24040:AF006823  
 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847  
 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839  
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592  
 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040  
 45 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247  
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089  
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT  
 [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214  
 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327  
 50 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600  
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236  
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868  
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295  
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344  
 R-HEMBA1003806//ESTs//0.00041:10204:100//Hs.100000:AA000000  
 R-HEMBA1003836//Smad-inducible cytokine Aa (RANTES)//3.2e-30:284:80//Hs.100000:AA000000  
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium  
 tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161  
 R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033  
 R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547  
 5 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911  
 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621  
 R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930  
 R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179  
 10 R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788  
 R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187  
 R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659  
 R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157  
 R-HEMBA1003939  
 R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669  
 15 R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545  
 R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591  
 R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562  
 R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253  
 R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525  
 20 R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882  
 R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:448:97//Hs.117834:AA766771  
 R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756  
 R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682  
 25 R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105  
 R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899  
 R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011  
 R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774  
 R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461  
 30 R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191  
 R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253  
 R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804  
 R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469  
 R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717  
 35 R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754  
 R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080  
 R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988  
 R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652  
 R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251  
 40 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918  
 R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562  
 R-HEMBA1004133  
 R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736  
 R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320  
 45 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219  
 R-HEMBA1004150//GRANULOCYTE INFLAMMATORY PROTEIN 1//0.99:357:59//Hs.79381:M81637  
 R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087  
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855  
 R-HEMBA1004199  
 50 R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701  
 R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.10092:AI189282  
 R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518  
 R-HEMBA1004225//EST//1.0:152:61//Hs.149093:AI243988  
 R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY Y SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-16:117:91//Hs.92033:AA255832

R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353  
 R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389  
 R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258  
 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus  
 5 norvegicus]//2.1e-61:221:86//Hs.7089:W37284  
 R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962  
 R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-  
 89:465:95//Hs.113660:D20018  
 R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931  
 10 R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:  
 AF091081  
 R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-  
 92:559:89//Hs.28298:AA203228  
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:  
 15 97//Hs.101766:AF022795  
 R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:  
 U13061  
 R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7  
 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961  
 20 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426  
 R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679  
 R-HEMBA1004321//Zinc finger protein 44 (KIX 7)//2.6e-37:415:64//Hs.51199:X16281  
 R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904  
 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714  
 25 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561  
 R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231  
 R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336  
 R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240  
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:  
 30 D89667  
 R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353  
 R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:  
 X77494  
 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869  
 35 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057  
 R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264  
 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084  
 R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219  
 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717  
 40 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:  
 AA648933  
 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.  
 12940:AI123518  
 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503  
 45 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829  
 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033  
 R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172  
 R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306  
 R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034  
 50 R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941  
 R-HEMBA1004507  
 R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTER-  
 GENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271  
 R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-  
 89:465:95//Hs.113660:D20018  
 R-HEMBA1004538//ESTs, Highly similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTER-  
 GENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271  
 R-HEMBA1004554  
 R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913  
 R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243  
 R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769  
 R-nnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661  
 5 R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970  
 R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915  
 R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785  
 10 R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152  
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393  
 R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454  
 R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442  
 15 R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348  
 R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560  
 R-HEMBA1004672//EST//6.7e-76:315:97//Hs.20821:R19368  
 R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252  
 R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562  
 20 R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042  
 R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881  
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219  
 R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235  
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer//2.1e-44:467:73//Hs.91916:AF035317  
 25 R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151  
 R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275  
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828  
 R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651  
 30 R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428  
 R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081  
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498  
 R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679  
 R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504  
 35 R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380  
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705  
 R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092  
 R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633  
 40 R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476  
 R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167  
 R-nnnnnnnnnnnn  
 R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732  
 R-HEMBA1004806  
 45 R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676  
 R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:M74002  
 R-HEMBA1004847  
 50 R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120  
 R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267  
 R-HEMBA1004864  
 R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362  
 R-HEMBA1004889//ESTs//4.8e-11:1496:97//Hs.15641:W6367  
 R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470  
 R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011  
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390

R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388  
 R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053  
 R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053  
 5 R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883  
 R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215  
 R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434  
 R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007  
 R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074  
 10 R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040  
 R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035  
 R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065  
 R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404  
 R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683  
 15 R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329  
 R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894  
 R-HEMBA1004995  
 R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520  
 20 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212  
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548  
 R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382  
 25 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067  
 R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348  
 R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//Hs.16258:AI376436  
 R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145  
 30 R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451  
 R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905  
 R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789  
 R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077  
 R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958  
 35 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:AF080561  
 R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739  
 R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952  
 R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173  
 40 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.67619:AB007957  
 R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:AF039694  
 R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397  
 45 R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914  
 R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766  
 R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239  
 R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:61//Hs.26931:AF061836  
 50 R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284  
 R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687  
 R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331  
 R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834  
 R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393895  
 R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//1.1e-44:304:83//Hs.85889:U17077  
 R-HEMBA1005274//ESTs//3.0e-65:322:98//Hs.105166:AA668861  
 R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391  
 R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

- R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750  
 R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219  
 R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519  
 R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046  
 5 R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169  
 R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472  
 R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606  
 R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467  
 R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.129735:AF010144  
 10 R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350  
 R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653  
 R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305  
 R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150  
 15 R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568  
 R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278  
 R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725  
 R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059  
 20 R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757  
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248  
 R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960  
 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391  
 25 R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961  
 R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494  
 R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353  
 R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:K00627  
 30 R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445  
 R-HEMBA1005497  
 R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788  
 R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544  
 35 R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870  
 R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:AI219740  
 R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322  
 R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045  
 40 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981  
 R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788  
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.17035:AI080471  
 R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350  
 45 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926  
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627  
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193  
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103  
 50 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709  
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497  
 R-HEMBA1005577  
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538  
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:Q06392  
 R-HEMBA1005583//ESTs//1.0e-100:510:96//Hs.9115:N90926  
 R-HEMBA1005588//Human mRNA//2.6e-52:403:83//Hs.155464:AF088219  
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905  
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125  
 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390  
 R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422  
 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.  
 5 19400:AA662845  
 R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:317:78//Hs.1721:X58377  
 R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081  
 R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522  
 R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.  
 10 10458:AF088219  
 R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973  
 R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477  
 R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450  
 R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258  
 15 R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:  
 U44060  
 R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//  
 1.7e-47:376:84//Hs.26988:U66406  
 R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055  
 20 R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943  
 R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:  
 AJ006470  
 R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815  
 R-NNNNNNNNNNNN//EST//0.098:125:68//Hs.136945:AA765672  
 25 R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096  
 R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:  
 U21936  
 R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974  
 R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.  
 30 10458:AF088219  
 R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601  
 R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960  
 R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201  
 R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618  
 35 R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911  
 R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917  
 R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970  
 R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252  
 R-HEMBA1005894  
 40 R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686  
 R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363  
 R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632  
 R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:  
 AB011098  
 45 R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867  
 R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418  
 R-HEMBA1005963  
 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.  
 26285:AF082516  
 50 R-HEMBA1005991//Human antiseecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199  
 R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618  
 R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875  
 R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436  
 R-NNNNNNNNNNNN//Homo sapiens mRNA for KIAA0725 protein, complete cds//1.1e-45:446:75//Hs.59403:  
 AB011098  
 R-HEMBA1006036//EST//1.4e-428:100//Hs.126771:AA416631  
 R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490  
 R-NNNNNNNNNNNN

- R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612  
 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517  
 R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313  
 5 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//  
 Hs.73614:U83460  
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297  
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293  
 R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931  
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635  
 10 R-HEMBA1006130//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:  
 AB007958  
 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542  
 R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212  
 R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930  
 15 R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627  
 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906  
 R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125  
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557  
 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//  
 20 Hs.23617:AA928683  
 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522  
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:  
 AF083384  
 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881  
 25 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.  
 10552:AA524401  
 R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:  
 92//Hs.104129:AA923278  
 R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.  
 30 cerevisiae]//1.6e-66:377:91//Hs.108674:W25821  
 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735  
 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019  
 R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037  
 35 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:  
 U33931  
 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:  
 AI204587  
 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219  
 40 R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184  
 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204  
 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075  
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382  
 45 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008  
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787  
 R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830  
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:  
 AB011166  
 50 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651  
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:582:84//Hs.23094:M19503  
 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923  
 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778  
 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.28514:U53204  
 R-HEMBA1006424//ESTs//1.2e-12:249:68//Hs.28514:U53204  
 R-HEMBA1006426//ESTs//1.2e-12:249:68//Hs.28514:U53204  
 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380  
 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784  
 R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895  
 R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]/3.0e-17:342:63//Hs.111730:AA604403  
 R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441  
 5 R-HEMBA1006474  
 R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984  
 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701  
 R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223  
 10 R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350  
 R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720  
 R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387  
 R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117  
 R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505  
 15 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566  
 R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300  
 R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628  
 R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934  
 20 R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331  
 R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154  
 R-HEMBA10065597//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]/1.8e-109:547:96//Hs.21122:AA191594  
 R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064  
 25 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876  
 R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725  
 R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876  
 R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280  
 30 R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390  
 R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219  
 R-HEMBA1006612  
 R-nnnnnnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247  
 R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630  
 35 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067  
 R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]/2.7e-91:426:100//Hs.139469:AI299889  
 R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]/3.4e-37:186:100//Hs.109818:AA411185  
 40 R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777  
 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282  
 R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427  
 R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511  
 45 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102  
 R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594  
 R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842  
 R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435  
 R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263  
 50 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695  
 R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]/1.1e-92:483:94//Hs.6525:AI205313  
 R-HEMBA1006709//ESTs//1.1e-100:536:93//Hs.142613:AA129427  
 R-HEMBA1006710//ESTs//1.1e-100:536:93//Hs.142613:AA129427  
 R-HEMBA1006737//ESTs//1.1e-100:536:93//Hs.142613:AA129427  
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627  
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099

R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646  
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763  
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881  
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562  
 5 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936  
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705  
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978  
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333  
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305  
 10 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272  
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556  
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087  
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:  
 15 AB018315  
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453  
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739  
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117  
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400  
 20 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308  
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712  
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382  
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:  
 AJ010841  
 25 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321  
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457  
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827  
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325  
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679  
 30 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440  
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293  
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363  
 R-HEMBA1007045  
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788  
 35 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839  
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140  
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272  
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866  
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-  
 40 40:163:83//Hs.152369:AA504818  
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087  
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025  
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597  
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272  
 45 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438  
 R-HEMBA1007147  
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818  
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674  
 R-nnnnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085  
 50 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954  
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051  
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987  
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990  
 R-HEMBA1007207//ESTs//1.6e-47:377:99//Hs.98912:AA436864  
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934  
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062  
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207  
 R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543  
 R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804  
 5 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990  
 R-HEMBA1007301  
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917  
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:AA205569  
 10 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629  
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452  
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848  
 15 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684  
 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333  
 R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403  
 R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090  
 20 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969  
 R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418  
 R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332  
 R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449  
 R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME  
 25 III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465  
 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928  
 R-HEMBA1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702  
 R-HEMBA1000044//EST//7.6e-70:367:95//Hs.140860:R42954  
 30 R-HEMBA1000048//EST//1.5e-45:262:91//Hs.157627:AI357802  
 R-HEMBA1000050//ESTs//0.039:91:74//Hs.163189:AA236903  
 R-HEMBA1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107  
 R-HEMBA1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-UNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584  
 35 R-HEMBA1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939  
 R-HEMBA1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997  
 R-HEMBA1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353  
 R-HEMBA1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193  
 R-HEMBA1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:AB014540  
 40 R-HEMBA1000113//EST//8.2e-94:437:100//Hs.136893:AA805239  
 R-HEMBA1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521  
 R-HEMBA1000136//ESTs//0.043:262:59//Hs.61304:AA025692  
 R-HEMBA1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915  
 45 R-HEMBA1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951  
 R-HEMBA1000173//EST//9.6e-44:258:76//Hs.161917:AA483223  
 R-HEMBA1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558  
 R-HEMBA1000198//ESTs//1.0:123:62//Hs.116602:AA665965  
 R-HEMBA1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353  
 50 R-HEMBA1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364  
 R-HEMBA1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019  
 R-HEMBA10002267//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME III [C. elegans]//5.1e-73:449:89//Hs.16803:AA843214  
 R-HEMBA1000244//ESTs, Small nucleolar cytosolic protein (RANES) [H.sapiens]//1.1e-44:341:71//Hs.111730:AA604403  
 R-HEMBA1000250//EST//8.8e-12:284:64//Hs.145960:AI276783  
 R-HEMBA1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

R-HEM BB1000264

R-HEM BB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]//2.7e-102:556:93//Hs.16079:AA083522

R-HEM BB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385

5 R-HEM BB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:AB011129

R-HEM BB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458

R-HEM BB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353

R-HEM BB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601

10 R-HEM BB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034

R-HEM BB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219

R-HEM BB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576

R-HEM BB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480

R-HEM BB1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084

15 R-HEM BB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219

R-HEM BB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736

R-HEM BB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651

R-HEM BB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020

R-HEM BB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008

20 R-HEM BB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590

R-HEM BB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.92381:AB007956

R-HEM BB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969

R-HEM BB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840

25 R-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642

R-HEM BB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173

R-HEM BB1000404//ESTs//0.088:298:59//Hs.61607:AA032026

R-HEM BB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591

R-HEM BB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087

30 R-HEM BB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//0.30:214:63//Hs.142209:AA873303

R-HEM BB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990

R-HEM BB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221

R-HEM BB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438

35 R-HEM BB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396

R-HEM BB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390

R-HEM BB1000487//EST//0.78:87:68//Hs.134601:AI081506

R-HEM BB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219

R-HEM BB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080

40 R-HEM BB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125

R-HEM BB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703

R-HEM BB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087

R-HEM BB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080

R-HEM BB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099

45 R-HEM BB1000550//EST//2.9e-11:113:79//Hs.161503:N68662

R-HEM BB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288

R-HEM BB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986

R-HEM BB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258

50 R-HEM BB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709

R-HEM BB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618

R-HEM BB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247

R-HEM BB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895

R-HEM BB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704

R-HEM BB1000592//ESTs//1.1e-40:406:75//Hs.138787:H73704

R-HEM BB1000598//Human secretory factor 1 mRNA, complete cds//1.1e-40:406:75//Hs.138787:H73704

R-HEM BB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125

R-HEM BB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

- R-HEM BB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152  
 R-HEM BB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531  
 R-HEM BB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522  
 R-HEM BB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582  
 5 R-HEM BB1000643//ESTs//0.0049:191:62//Hs.55445:W31963  
 R-HEM BB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100  
 R-HEM BB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939  
 R-HEM BB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988  
 R-HEM BB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705  
 10 R-HEM BB1000673//EST//0.58:46:82//Hs.142286:AA338293  
 R-HEM BB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454  
 R-nnnnnnnnnnnnn/Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723  
 R-HEM BB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219  
 R-HEM BB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412  
 15 R-HEM BB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403  
 R-HEM BB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306  
 R-HEM BB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881  
 R-HEM BB1000738//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272  
 R-HEM BB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925  
 20 R-HEM BB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522  
 R-HEM BB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445  
 R-HEM BB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541  
 R-HEM BB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771  
 R-HEM BB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193:75//Hs.73734:Z23091  
 25 R-HEM BB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718  
 R-HEM BB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961  
 R-HEM BB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219  
 R-HEM BB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447  
 R-HEM BB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124  
 30 R-HEM BB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219  
 R-HEM BB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881  
 R-HEM BB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176  
 R-HEM BB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545  
 R-HEM BB1000840//ATPase, Na<sup>+</sup>/K<sup>+</sup> transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876  
 35 R-HEM BB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137  
 R-HEM BB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599  
 R-HEM BB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942  
 R-HEM BB1000876//EST//0.0022:211:63//Hs.125552:AA884141  
 40 R-HEM BB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247  
 R-HEM BB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740  
 R-HEM BB1000888//EST//8.2e-07:196:64//Hs.118276:W15258  
 R-HEM BB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327:83//Hs.51048:X68830  
 R-HEM BB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881  
 45 R-HEM BB1000908//EST//0.95:27:100//Hs.142568:AA285066  
 R-HEM BB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983  
 R-HEM BB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325  
 R-HEM BB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742  
 R-HEM BB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874  
 50 R-HEM BB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784  
 R-HEM BB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881  
 R-HEM BB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:MI9503  
 R-HEM BB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354  
 R-HEM BB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007  
 R-HEM BB1000985//ESTs//1.1e-100:524:95//Hs.43102:AA111194  
 R-HEM BB1000991//EST//0.99:58:72//Hs.100246:T23625  
 R-HEM BB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

- R-HEM BB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112  
 R-HEM BB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:H58762  
 R-HEM BB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214  
 5 R-HEM BB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814  
 R-HEM BB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080  
 R-HEM BB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562  
 R-HEM BB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385  
 R-HEM BB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975  
 10 R-HEM BB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107  
 R-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:AB014518  
 R-HEM BB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944  
 15 R-HEM BB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785  
 R-HEM BB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381  
 R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803  
 R-HEM BB1001096//Human HsLIM15 mRNA for HsLIM15, complete cds//1.2e-20:233:70//Hs.37181:D64108  
 R-HEM BB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353  
 20 R-HEM BB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080  
 R-HEM BB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426  
 R-HEM BB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092  
 R-HEM BB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942  
 R-HEM BB1001126  
 25 R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077  
 R-HEM BB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
 R-HEM BB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881  
 R-HEM BB1001151  
 30 R-HEM BB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197  
 R-HEM BB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878  
 R-nnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162  
 R-HEM BB1001177  
 35 R-HEM BB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349  
 R-HEM BB1001199  
 R-HEM BB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183  
 R-HEM BB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549  
 R-HEM BB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573  
 40 R-HEM BB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody I4A))/3.1e-44:298:87//Hs.103458:X53795  
 R-HEM BB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817  
 R-HEM BB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//Hs.71873:AA148213  
 45 R-HEM BB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560  
 R-HEM BB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236  
 R-HEM BB1001253//EST//0.0011:84:77//Hs.124579:AA853987  
 R-HEM BB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268  
 R-HEM BB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970  
 50 R-HEM BB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087  
 R-HEM BB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412  
 R-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III (nematostella elegans) //3.0e-10:10:10//Hs.16636:W81281  
 R-HEM BB1001289//ESTs//1.0e-45:440:75//Hs.44702:AI14884  
 R-HEM BB1001294//ESTs//1.0e-40:476:99//Hs.109017:AI057  
 R-HEM BB1001302  
 R-HEM BB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

R-HEM BB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627  
 R-HEM BB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627  
 R-HEM BB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873  
 5 R-HEM BB1001326//ESTs//0.85:174:62//Hs.133487:AI393754  
 R-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222  
 R-HEM BB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365  
 R-HEM BB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639  
 R-HEM BB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470  
 10 R-HEM BB1001346  
 R-HEM BB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354  
 R-HEM BB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721  
 R-HEM BB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055  
 15 R-HEM BB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087  
 R-HEM BB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617  
 R-HEM BB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219  
 R-HEM BB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205  
 R-HEM BB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699  
 20 R-HEM BB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970  
 R-HEM BB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350  
 R-HEM BB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.68:365:58//Hs.389:X76342  
 R-HEM BB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644  
 R-HEM BB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651  
 25 R-HEM BB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846  
 R-HEM BB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317  
 R-HEM BB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201  
 R-HEM BB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236  
 R-HEM BB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515  
 30 R-HEM BB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293  
 R-HEM BB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881  
 R-HEM BB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468  
 R-HEM BB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481  
 R-HEM BB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515  
 35 R-HEM BB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280  
 R-HEM BB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915  
 R-HEM BB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159  
 40 R-HEM BB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459  
 R-HEM BB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353  
 R-HEM BB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869  
 R-HEM BB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274  
 R-HEM BB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962  
 45 R-HEM BB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521  
 R-HEM BB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329  
 R-HEM BB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944  
 R-HEM BB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219  
 R-HEM BB1001588//EST//8.3e-27:363:69//Hs.141603:N66015  
 50 R-HEM BB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184  
 R-HEM BB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044  
 R-HEM BB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888  
 R-HEM BB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272  
 R-HEM BB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082  
 R-HEM BB1001641//EST//2.4e-15:67:86//Hs.162398:AA57281  
 R-HEM BB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438  
 R-HEM BB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

- R-HEM BB1001668//ESTs//0.73:212:62//Hs.8928:N32572  
 R-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439:AB014546  
 R-HEM BB1001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534  
 5 R-HEM BB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358  
 R-HEM BB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867  
 R-HEM BB1001704//EST//0.96:248:57//Hs.163025:AA703038  
 R-HEM BB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080  
 10 R-HEM BB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:AA205569  
 R-HEM BB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645  
 R-HEM BB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113  
 15 R-HEM BB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403  
 R-HEM BB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488  
 R-HEM BB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287  
 R-HEM BB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059  
 R-HEM BB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211  
 20 R-HEM BB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008:L00352  
 R-HEM BB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369  
 R-HEM BB1001785//ESTs//0.040:390:58//Hs.116651:AA993406  
 R-HEM BB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253  
 25 R-HEM BB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391  
 R-HEM BB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247  
 R-HEM BB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503  
 R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209  
 30 R-HEM BB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.67619:AB007957  
 R-HEM BB1001839  
 R-HEM BB1001850//EST//0.020:119:68//Hs.32767:H38125  
 R-HEM BB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539  
 35 R-HEM BB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106  
 R-HEM BB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397  
 R-HEM BB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434  
 R-HEM BB1001872//EST//0.85:156:64//Hs.119501:AA487980  
 R-HEM BB1001874//EST//0.64:107:70//Hs.147482:AI215572  
 40 R-HEM BB1001875//EST//0.079:199:59//Hs.121810:AA775240  
 R-HEM BB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081  
 R-HEM BB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310  
 R-HEM BB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191  
 R-HEM BB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725  
 45 R-HEM BB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915  
 R-HEM BB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216  
 R-HEM BB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750  
 R-HEM BB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897  
 R-HEM BB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390  
 50 R-HEM BB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRp129//7.4e-38:531:70//Hs.153086:Y11251  
 R-HEM BB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325  
 R-HEM BB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875  
 R-HEM BB1001944//EST//1.0e-104:178:81//Hs.92664:N23366  
 R-HEM BB1001945//ESTs//1.0e-104:178:81//Hs.92664:N23366  
 R-HEM BB1001946//ESTs//1.0e-104:178:81//Hs.92664:N23366  
 R-HEM BB1001947//ESTs//1.0e-104:178:81//Hs.92664:N23366  
 R-HEM BB1001948//ESTs//1.0e-104:178:81//Hs.92664:N23366  
 R-HEM BB1001949//ESTs//1.0e-104:178:81//Hs.92664:N23366  
 R-HEM BB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998  
 R-HEM BB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

- R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522  
 R-HEM BB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881  
 R-HEM BB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972  
 R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:  
 5 AB011147  
 R-HEM BB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531  
 R-HEM BB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475  
 R-HEM BB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572  
 R-HEM BB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223  
 10 R-HEM BB1001996  
 R-HEM BB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798  
 R-HEM BB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:  
 K00627  
 R-HEM BB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334  
 15 R-HEM BB1002009//EST//2.9e-44:245:94//Hs.28788:R66896  
 R-HEM BB1002015//EST//0.0027:198:63//Hs.160868:AI359052  
 R-HEM BB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900  
 R-HEM BB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426  
 R-HEM BB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638  
 20 R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080  
 R-HEM BB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638  
 R-HEM BB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840  
 R-HEM BB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671  
 R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.  
 25 129735:AF010144  
 R-HEM BB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193  
 R-HEM BB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881  
 R-HEM BB1002115  
 R-HEM BB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814  
 30 R-HEM BB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 1.4e-45:281:88//Hs.125231:AF068006  
 R-HEM BB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553  
 R-HEM BB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073  
 R-HEM BB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185  
 35 R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934  
 R-HEM BB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881  
 R-HEM BB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841  
 R-HEM BB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584  
 R-HEM BB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631  
 40 R-HEM BB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807  
 R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503  
 R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363  
 R-HEM BB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112  
 R-HEM BB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223  
 45 R-HEM BB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305  
 R-HEM BB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892  
 R-HEM BB1002327//EST//0.042:249:61//Hs.121097:AA714637  
 R-HEM BB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312  
 R-HEM BB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228  
 50 R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841  
 R-HEM BB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322  
 R-HEM BB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613  
 R-HEM BB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522  
 R-HEM BB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085  
 R-HEM BB1002383//ESTs//3.0e-18:51:98//Hs.45140:D80051  
 R-HEM BB1002387  
 R-HEM BB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:

168:77//Hs.133526:N21103

R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280

R-HEMBB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293

5 R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353

R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087

R-HEMBB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089

R-HEMBB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083

R-HEMBB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176

10 R-HEMBB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969

R-HEMBB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017

R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142

R-HEMBB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615

R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278

15 R-HEMBB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538

R-HEMBB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672

R-HEMBB1002531//EST//0.024:147:61//Hs.148305:AA909605

R-HEMBB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478

20 R-HEMBB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259

R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:T68813

R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.9e-45:344:82//Hs.51048:X68830

R-HEMBB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189

25 R-HEMBB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045

R-HEMBB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138

R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087

R-HEMBB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424

R-HEMBB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923

30 R-HEMBB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881

R-HEMBB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896

R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265

R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977

35 R-HEMBB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150

R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917

R-HEMBB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247

40 R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219

R-HEMBB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881

R-HEMBB1002677//ESTs//0.65:159:62//Hs.163517:AI419775

R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:Z28339

45 R-HEMBB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646

R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753

R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099

R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487

R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398

50 R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842

R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547

R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682

R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701

R-MAMMA1000019//Small inducible cytokine A5 (RANTES) [H.sapiens]

R-MAMMA1000020//Small inducible cytokine A5 (RANTES) [H.sapiens]

R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:104:77//Hs.3251:AB007400

R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304

R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165  
 R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350  
 R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531  
 5 R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065  
 R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099  
 R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241  
 R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713  
 10 R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352  
 R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172  
 15 R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577  
 R-MAMMA1000133  
 R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017  
 R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970  
 20 R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881  
 R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.17579:AF013263  
 R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787  
 R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:  
 25 AJ224162  
 R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069  
 R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611  
 R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054  
 30 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881  
 R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398:AA421103  
 R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425  
 R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946  
 35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315  
 R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090  
 R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041  
 40 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238  
 R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814  
 R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977  
 R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369  
 45 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694  
 R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956  
 R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000287  
 50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892  
 R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067  
 R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251  
 R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434  
 R-MAMMA1000313//EST//8.3e-19:294:62//Hs.107400:AA964401  
 R-MAMMA1000314//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000315//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000316//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000317//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000318//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000319//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000320//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000321//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000322//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000323//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000324//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000325//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000326//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000327//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000328//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000329//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000330//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000331//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000332//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000333//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000334//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000335//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000336//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000337//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000338//EST//1.1e-10:151:73//Hs.60742:AA017066  
 R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881  
 R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159  
 R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912  
 R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087  
 5 R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659  
 R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523  
 R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065  
 R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132  
 10 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060  
 R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973  
 R-MAMMA1000410//Archaea//1.8e-40:443:74//Hs.33642:X81198  
 R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958  
 15 R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099  
 R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171  
 R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081  
 20 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067  
 R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390  
 R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452  
 R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461  
 25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171  
 R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179  
 R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447  
 R-MAMMA1000458  
 30 R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176  
 R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361  
 R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959  
 R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886  
 R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759  
 35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219  
 R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390  
 R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390  
 R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267  
 R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236  
 40 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131  
 R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561  
 R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211  
 R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872  
 R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548  
 45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219  
 R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042  
 R-MAMMA1000605//CD4 receptor [exons 1 and 2] [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267  
 R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105  
 50 R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180  
 R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361  
 R-MAMMA1000623  
 R-MAMMA1000625//ESTs//1.0e-90:477:94//Hs.26073:R96361  
 R-MAMMA1000643//ESTs//1.0e-90:477:94//Hs.26073:R96361  
 R-MAMMA1000664//Homo sapiens mRNA for putative lipid acid synthetase, partial cds//2e-43:400:76//Hs.5555:AJ224162  
 R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]/8.4e-98:464:98//Hs.31431:AI022065  
R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476  
R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212  
5 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343  
R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644  
R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333  
R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]/1.2e-29:158:79//Hs.142764:AA205569  
10 R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515  
R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329  
R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942  
R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267  
15 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893  
R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]/1.2e-35:371:74//Hs.141429:AA631915  
R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141  
R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]/2.3e-116:557:98//Hs.71472:AA632288  
20 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205  
R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503  
R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627  
R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131  
25 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256  
R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353  
R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204  
R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439  
R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150  
30 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163  
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)/1.5e-45:358:76//Hs.73919:X81637  
R-MAMMA1000831//ESTs//1.3e-1,04:510:97//Hs.17494:AA572675  
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881  
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902  
35 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/9.4e-44:363:79//Hs.96337:AA225358  
R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097  
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955  
R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251  
40 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390  
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212  
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311  
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922  
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099  
45 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399  
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875  
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243  
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128  
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166  
50 R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107  
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215  
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329  
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017097  
R-MAMMA1000908//ESTs//1.0e-12:109:67//Hs.38559:AA731604  
R-MAMMA1000914//ESTs//1.2e-150:63//Hs.119162:AA399989  
R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696

- R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335  
 R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727  
 R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281  
 R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428  
 5 R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053  
 R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178  
 R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//7.5e-49:340:85//Hs.103458:X53795  
 10 R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:AB011147  
 R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881  
 R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204  
 R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:AB018304  
 15 R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881  
 R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263  
 R-MAMMA1001003//Sialoporphin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075  
 20 R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313  
 R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333  
 R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814  
 R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536  
 R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461  
 25 R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390  
 R-nnnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650  
 R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881  
 R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:AI015487  
 30 R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532  
 R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748  
 R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353  
 R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944  
 R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503  
 35 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222  
 R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926  
 R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587  
 R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686  
 40 R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576  
 R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267  
 R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750  
 45 R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029  
 R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399  
 R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179  
 R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131  
 R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750  
 50 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970  
 R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251  
 R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959  
 R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519  
 R-MAMMA1001198//ESTs, Weakly similar to nucleoside diphosphate kinase 1 [H.sapiens]//1.0e-44:333:78//Hs.107657:AA126814  
 R-MAMMA1001202//ESTs//1.0e-43:230:95//Hs.19788:AA521340  
 R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637  
 R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293  
 R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202  
 R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315  
 R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701  
 5 R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619  
 R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307  
 R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569  
 R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149  
 10 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561  
 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001  
 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643  
 15 R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144  
 R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371  
 R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876  
 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135  
 20 R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426  
 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984  
 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709  
 25 R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471  
 R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426  
 R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519  
 R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127  
 30 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478  
 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322  
 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216  
 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881  
 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831  
 35 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275  
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957  
 R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267  
 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168  
 40 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618  
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892  
 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542  
 R-MAMMA1001465  
 R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317  
 45 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394  
 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065  
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522  
 R-MAMMA1001510  
 50 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242  
 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969  
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696  
 R-MAMMA1001575//ESTs//1.3e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001576//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001577//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001578//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001579//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001580//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001581//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001582//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001583//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001584//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001585//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001586//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001587//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001588//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001589//ESTs//1.1e-20:440:98//Hs.162882:AA807315  
 R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441  
 R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

R-MAMMA1001604

R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]/1.9e-97:488:96//Hs.143263:AI057616

R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272

5 R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315

R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]/6.8e-15:168:73//Hs.115216:AA291074

R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377

R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606

10 R-MAMMA1001649

R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144

R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219

R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248

15 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550

R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081

R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957

R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884

20 R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088

R-MAMMA1001715//ESTs//1.2e-73:399:9311Hs.124620:AI082338

R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596

R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]/3.7e-110:552:96//Hs.6923:AI161158

25 R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651

R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666

R-MAMMA1001744

R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817

R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041

30 R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413

R-MAMMA1001757//ESTs//1.0e-9.8:488:96//Hs.45184:C14904

R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276

R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847

R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325

35 R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825

R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]/7.6e-43:257:91//Hs.7634:AA481246

R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460

40 R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238

R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644

R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744

R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313

R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892

45 R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659

R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979

R-MAMMA1001818

R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881

R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519

50 R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140

R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394

R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811

R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461

R-MAMMA1001858//ESTs//1.4e-44:331:83//Hs.44702:AI148841

R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-37:262:77//Hs.576:AB007944

R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:

AF039694

R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942

5 R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795

10 R-nnnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI251374

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

15 R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]/6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219

20 R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

25 R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

30 R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]/4.0e-45:404:7811Hs/138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

35 R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

40 R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

45 R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

50 R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956

R-MAMMA1002215//ESTs//1.3e-30:134:65//Hs.145333:AI251374

R-MAMMA1002215//ESTs//1.3e-30:134:65//Hs.145333:AI251374

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696

R-MAMMA1002236

R-MAMMA1002243

5 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080

R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript

KIAA0487//1.6e-54:207:81//Hs.92381:AB007956

R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283

R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772

10 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141

R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751

R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982

R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881

15 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454

R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153

R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359

R-MAMMA1002308

20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452

R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:MI9503

R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094

R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:AF057280

25 R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183

R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084

R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658

R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317

30 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897

R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618

R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439

R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127

R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228

35 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390

R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367

R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73919:X81637

R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080

R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475

40 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587

R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236

R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542

R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219

45 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061

R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845

R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294

R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488

50 R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588

R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477

R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475

R-MAMMA1002434//ESTs, Moderately similar to HLA A11, SUBFAM 1, CDW34, A11, A11.1, A11.2, A11.3, A11.4, A11.5, A11.6, A11.7, A11.8, A11.9, A11.10, A11.11, A11.12, A11.13, A11.14, A11.15, A11.16, A11.17, A11.18, A11.19, A11.20, A11.21, A11.22, A11.23, A11.24, A11.25, A11.26, A11.27, A11.28, A11.29, A11.30, A11.31, A11.32, A11.33, A11.34, A11.35, A11.36, A11.37, A11.38, A11.39, A11.40, A11.41, A11.42, A11.43, A11.44, A11.45, A11.46, A11.47, A11.48, A11.49, A11.50, A11.51, A11.52, A11.53, A11.54, A11.55, A11.56, A11.57, A11.58, A11.59, A11.60, A11.61, A11.62, A11.63, A11.64, A11.65, A11.66, A11.67, A11.68, A11.69, A11.70, A11.71, A11.72, A11.73, A11.74, A11.75, A11.76, A11.77, A11.78, A11.79, A11.80, A11.81, A11.82, A11.83, A11.84, A11.85, A11.86, A11.87, A11.88, A11.89, A11.90, A11.91, A11.92, A11.93, A11.94, A11.95, A11.96, A11.97, A11.98, A11.99, A11.100, A11.101, A11.102, A11.103, A11.104, A11.105, A11.106, A11.107, A11.108, A11.109, A11.110, A11.111, A11.112, A11.113, A11.114, 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89121:AB007954

R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076

R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [*Saccharomyces cerevisiae*]//8.5e-104:544:93//Hs.94570:AI192106

5 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496

R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103

10 R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:AF055460

R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293

R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664

R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277

15 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214

R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147

R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851

20 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058

R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681

R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693

R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433

25 R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371

R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258

R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//Hs.1360:M29874

R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737

30 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369

R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053

R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389

R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670

35 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306

R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081

R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881

R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs.93332:AA811920

40 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.115325:D84488

R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390

R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421

R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915

45 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776

R-MAMMA1002655

R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886

R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087

50 R-MAMMA1002671//ESTs, Weakly similar to coded for by *C. elegans* cDNA yk52e10.5 [*C. elegans*]//5.3e-108:544:96//Hs.16464:W19606

R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213

R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:D86987

R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385

R-MAMMA1002686//EST//1.1e-31:223:86//Hs.112540:AA601385

R-MAMMA1002699//ESTs//3.1e-41:104:100//Hs.1026049:F2251

R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-71:353:96//Hs.138404:R70986

R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234  
 R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858  
 R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333  
 R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571  
 5 R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219  
 R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757  
 R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907  
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.154069:U06452  
 10 R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776  
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 R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651  
 15 R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272  
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 R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145  
 R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812  
 R-MAMMA1002807//Archair//1.4e-39:315:80//Hs.33642:X81198  
 20 R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260  
 R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319  
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 R-MAMMA1002835  
 R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723  
 25 R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395  
 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238  
 R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081  
 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067  
 R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941  
 30 R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592  
 R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194  
 R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871  
 R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219  
 R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811  
 35 R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783  
 R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915  
 R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087  
 R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179  
 40 R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002  
 R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881  
 R-MAMMA1002938  
 R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503  
 R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243  
 45 R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353  
 R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081  
 R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630  
 R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835  
 R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279  
 50 R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019  
 R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179  
 R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857  
 R-MAMMA1003007//ESTs//1.0e-104:80:44:48314:BA96611  
 R-MAMMA1003017//ESTs//1.0e-104:80:44:48314:BA96611  
 R-MAMMA1003018//ESTs//1.0e-104:80:44:48314:BA96611  
 R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315  
 R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358  
 R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321  
 5 R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160  
 R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940  
 R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941  
 R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862  
 R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348  
 10 R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881  
 R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559  
 R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:AA878911  
 R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969  
 15 R-MAMMA1003089//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652  
 R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651  
 R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283  
 R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366  
 20 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788  
 R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125  
 R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537  
 R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861  
 25 R-nnnnnnnnnnnnn  
 R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//Hs.6884:W30736  
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640  
 R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312  
 30 R-NT2RM4000027  
 R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663  
 R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI86169  
 R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379  
 R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e-113:549:97//Hs.95665:AF070639  
 35 R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817  
 R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708  
 R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312  
 R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-99:536:92//Hs.127810:AI246301  
 40 R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397  
 R-nnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962  
 R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160  
 R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113  
 45 R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723  
 R-NT2RM4000199//ESTs//10.020:95:651//Hs.146203:AI254528  
 R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876  
 R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219  
 R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:AB018255  
 50 R-NT2RM4000215  
 R-nnnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760  
 R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor)  
 R-NT2RM4000244//ESTs//0.020:95//Hs.18646:AA6133  
 R-NT2RM4000251//Homo sapiens mRNA for RIP6 (thyroid receptor interacting protein)//0.002:462:111  
 119498:AF000974  
 R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742



R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891  
 R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520  
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:  
 M21868  
 5 R-NT2RM4000813  
 R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:  
 AI219667  
 R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031  
 R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864  
 10 R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597  
 R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343  
 R-nnnnnnnnnnnnn  
 R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-  
 96:450:99//Hs.142076:AA604514  
 15 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262  
 R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887  
 R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647  
 R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:  
 AA650126  
 20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:  
 AB018272  
 R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:  
 AB014539  
 R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352  
 25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.  
 32170:AB015132  
 R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300  
 R-nnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798  
 R-NT2RM4001092//ESTs//1.4e-86:517:89//Hs.132969:Z78324  
 30 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962  
 R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276  
 R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311  
 R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848  
 R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085  
 35 R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-  
 43:273:91//Hs.109005:N31174  
 R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942  
 R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849  
 R-NT2RM4001203  
 40 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307  
 R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410  
 R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677  
 R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184  
 R-NT2RM4001309  
 45 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857  
 R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899  
 R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352  
 R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.  
 18442:AI129307  
 50 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339  
 R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476  
 R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211  
 R-NT2RM4001382  
 R-NT2RM4001384//EST//3.6e-51:145:98//Hs.55000:AA8355  
 R-NT2RM4001411//EST//1.1e-90:436:99//Hs.95900:AA160339  
 R-NT2RM4001412//EST//0.17:186:61//Hs.16751:T90476  
 94//Hs.15744:AI055859  
 R-NT2RM4001412



R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178  
 R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.2e-105:  
 535:95//Hs.30991:AA994438  
 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143  
 5 R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893  
 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:  
 AF098162  
 R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268  
 R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]/5.7e-62:326:95//Hs.3385:N25917  
 10 R-ntnnnnnnnnnnr/ESTs, Weakly similar to IP63 protein [R.norvegicus]/1.9e-21:121:98//Hs.8772:AA521097  
 R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265  
 R-NT2RM4001984  
 R-NT2RM4001987  
 R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528  
 15 R-NT2RM4002018  
 R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087  
 R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435  
 R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226  
 R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887  
 20 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179  
 R-ntnnnnnnnnnnr/Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:  
 AF071309  
 R-NT2RM4002067//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629  
 R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]/6.8e-57:290:96//  
 25 Hs.109274:AA193416  
 R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655  
 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528  
 R-ntnnnnnnnnnnr/ESTs//1.0:95:69//Hs.25897:W65409  
 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620  
 30 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712  
 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987  
 R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090  
 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535  
 R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258  
 35 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400  
 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343  
 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678  
 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079  
 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
 40 //5.1e-112:569:95//Hs.23900:U82984  
 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglu-  
 cosaminyltransferase [C.elegans]/1.1e-100:544:93//Hs.27567:W72190  
 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219  
 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864  
 45 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263  
 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638  
 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461  
 R-NT2RM4002294  
 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164  
 50 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498  
 R-ntnnnnnnnnnnr/ESTs//5.0e-59:283:100//Hs.125048:AA682913  
 R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198  
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:  
 AF071540  
 R-NT2RM4002374//ESTs//2.7e-43:455:97//Hs.134278:AA648864  
 R-NT2RM4002383//ESTs//2.7e-43:455:97//Hs.134278:AA648864  
 R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328  
 R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]/1.3e-97:473:

98//Hs.16464:W19606

R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677

R-NT2RM4002446

R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142

R-NT2RM4002457

R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890

R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.8765:AF083255

R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:AB014591

R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884

R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029

R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464

R-nnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//Hs.31030:H50467

R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788

R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057

R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312

R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE [Bos taurus]//2.3e-89:435:97//Hs.15830:AA165698

R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569

R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//9.6e-28:194:87//Hs.59346:AI126802

R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096

R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081

R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115

R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713

R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290

R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749

R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798

R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910

R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793:AA775879

R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881

R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097

R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.54877:AF050078

R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.102576:AJ010230

R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338

R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064

R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757

R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827

R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419

R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356

R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//1.9e-19:153:86//Hs.5268:W22670

R-nnnnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099

R-nnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513

R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-89:457:95//Hs.3832:AI208601

R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548

R-NT2RP2000154//ESTs//1.0e-74:375:96//Hs.105061:N45096

R-NT2RP2000155//ESTs//1.0e-74:375:96//Hs.105061:N45096

R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI14374

R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373

R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510

R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.4e-80:415:95//Hs.11807:T86897

R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382

R-NT2RP2000232

5 R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683

R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379

R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]/1.3e-95:454:99//Hs.102057:AA649005

R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840

10 R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649

R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]/8.4e-59:298:96//Hs.16085:AI261382

R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635

R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865

15 R-NT2RP2000289

R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]/9.8e-106:494:99//Hs.102951:AA574249

R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712

R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381

20 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase I, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398

25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]/3.4e-69:371:94//Hs.43436:N32441

R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981

30 R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103

R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010

R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265

35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]/1.3e-65:362:93//Hs.22197:AI151425

R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]/3.6e-75:435:92//Hs.21938:W81045

R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013

R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078

40 R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215

R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896

R-nnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348

R-NT2RP2000523

R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144

45 R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446

R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514

R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222

R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275

R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396

50 R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767

R-NT2RP2000678//ESTs//2.6e-53:271:96//Hs.23790:N99347

R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368

R-NT2RP2000715//EST//1.2e-87:418:99//Hs.139425:AA429279

R-NT2RP2000731//EST//5.2e-65:322:97//Hs.136754:AA712965

R-NT2RP2000738//EST//1.1e-64:322:97//Hs.136754:AA712965

R-NT2RP2000764//EST//1.1e-64:322:97//Hs.136754:AA712965

R-NT2RP2000809

R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

R-nnnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404  
 R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918  
 R-NT2RP2000819  
 R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511  
 5 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6  
 PRECURSOR//4.6e-10:247:66//Hs.29352:M31165  
 R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552  
 R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345  
 R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:  
 10 AB018284  
 R-NT2RP2000892//ESTs//2.8e-50:25 8:96//Hs.119238:AA476267  
 R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266  
 R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III  
 [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477  
 15 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:  
 AB018298  
 R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021  
 R-NT2RP2000970//EST//8-7e-06:255:62//Hs.149202:AI246481  
 R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC  
 20 REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537  
 R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521  
 R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643  
 R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660  
 R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108  
 25 R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665  
 R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068  
 R-NT2RP2001119  
 R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348  
 R-NT2RP2001137  
 30 R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512  
 R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145  
 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:  
 AB007949  
 R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287  
 35 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510  
 R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402  
 R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358  
 R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//  
 Hs.44014:AA632298  
 40 R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996  
 R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353  
 R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229  
 R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775  
 R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665  
 45 R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205  
 R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//  
 2.3e-43:238:93//Hs.106632:N25679  
 R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138  
 R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178  
 50 R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028  
 R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038  
 R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.  
 sapiens]//3.9e-74:411:93//Hs.47305:AA195153  
 R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001395//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001396//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001397//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001398//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001399//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001400//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001401//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001402//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001403//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001404//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001405//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001406//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001407//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001408//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001409//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001410//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001411//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001412//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001413//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001414//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001415//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001416//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001417//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001418//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001419//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001420//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001421//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001422//ESTs//1.1e-54:305:93//Hs.70256:R07875  
 R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

- R-NT2RP2001427//EST//1.7e-1 1:107:84//Hs.148584:AI201728  
 R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558:97//Hs.7627:AI341556  
 R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394  
 R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453  
 5 R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765  
 R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539  
 R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:AF088219  
 R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513  
 R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146  
 10 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545:95//Hs.4277:Y14494  
 R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240  
 R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586  
 15 R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816  
 R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387:96//Hs.67619:AB007957  
 R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:D14661  
 R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884  
 20 R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995  
 R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767  
 R-NT2RP2001613  
 R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294  
 R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090  
 25 R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845  
 R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336  
 R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323  
 R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579  
 R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538  
 30 R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100  
 R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840  
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:AF091754  
 R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037  
 35 R-NT2RP2001861  
 R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941  
 R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088  
 R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:AA113849  
 40 R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724  
 R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423  
 R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268  
 R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087  
 R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180  
 45 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594  
 R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588  
 R-NT2RP2001969  
 R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745  
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:89//Hs.18760:AA166678  
 50 R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233  
 R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332  
 R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627  
 R-NT2RP2002041  
 R-NT2RP2002047//ESTs//1.1e-45:145:95//Hs.16750:AA62989  
 R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068  
 R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091

R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265  
R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:87//Hs.11039:AF052183  
R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524  
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376:89//Hs.155218:  
AJ007509  
R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000  
R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134  
R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527  
R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268  
R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495  
R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269:98//Hs.107201:W52859  
R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-  
15:245:71//Hs.87578:AI125363  
R-NT2RP2002193//ESTs//3.5e-79:45 3:90//Hs.76578:AI290672  
R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946  
R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499  
R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341  
R-nnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:  
AA188168  
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:  
AF005418  
R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//Hs.92137:M19720  
R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550:91//Hs.4029:Z78373  
R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482:93//Hs.5570:AI377863  
R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527:94//  
Hs.24812:AF069532  
R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015  
R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:  
95//Hs.31034:AB015594  
R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372  
R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:  
89//Hs.109051:AF038958  
R-NT2RP2002394//ESTs//0.11:158:65//Hs.28792:AI343467  
R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815  
R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:80//Hs.15731:  
AB011135  
R-NT2RP2002439//ESTs//3.2e-12:134:76//Hs.32246:AA464020  
R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521  
R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230  
R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233  
R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605:92//Hs.  
125856:AB005289  
R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180  
R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838  
R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:91//Hs.23255:  
AB018334  
R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305  
R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090  
R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109:570:93//Hs.49476:AF009314  
R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325  
R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564:97//Hs.94549:  
AA149547  
R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783  
R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170  
R-NT2RP2002618//ESTs//1.1e-44:443:57//Hs.96322:AA541611  
R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881  
R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

R-NT2RP2002672

R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184:63//Hs.50727:U43572

R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223

R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210

5 R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626

R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300

R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108

R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352

R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131

10 R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042

R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124

R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537

R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124

15 R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578

R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031

R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870

R-NT2RP2002880

20 R-NT2RP2002891

R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894

R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143

R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096

R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771

25 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480

R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060

R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213

R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291

30 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329

R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.86337:AA149311

R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642

R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594

35 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082

R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081

R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512

R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345

R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355

40 R-NT2RP2003125

R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986

R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506

R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379

R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067

45 R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952

R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156

R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816

R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074

R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253

50 R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661

R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438

R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937

R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859

R-NT2RP2003277//Human mRNA for KIAA0625 gene, complete cds//1.0:100:100//Hs.107201:W52859

R-NT2RP2003280//ESTs//1.8e-104:497:98//Hs.113052:AI222106

R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106

R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087

R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321  
 R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874  
 R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [*Drosophila melanogaster*]//4.8e-109:553:96//Hs.26089:AA195126  
 5 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948  
 R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618  
 R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825  
 R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014  
 R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476  
 10 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502  
 R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249  
 R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683  
 R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [*Canis familiaris*]//1.2e-106:508:98//Hs.131840:AI016073  
 15 R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//5.6e-21:161:70//Hs.43153:N22360  
 R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [*C.elegans*]//6.0e-105:529:96//Hs.8055:W60903  
 R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332  
 R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121  
 20 R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [*D.melanogaster*]//7.0e-71:365:95//Hs.101056:R52777  
 R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [*S.cerevisiae*]//2.3e-115:577:96//Hs.16277:N36831  
 R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733  
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270  
 25 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783  
 R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170  
 R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101  
 R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684  
 30 R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//1.8e-58:316:94//Hs.28891:W72439  
 R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696  
 R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719  
 R-NT2RP2003596//ESTs, Weakly similar to No definition line found [*C.elegans*]//4.7e-101:495:98//Hs.34627:AA126463  
 35 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067  
 R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981  
 R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC REGION [*E.coli*]//9.1e-62:359:92//Hs.12492:AA203188  
 40 R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951  
 R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523  
 R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [*C.elegans*]//1.0:202:62//Hs.65539:AI148540  
 R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [*R.norvegicus*]//4.3e-99:492:96//Hs.93332:AA811920  
 45 R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097  
 R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401  
 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003  
 50 R-ntntntntntntntntntntnt//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:U18914  
 R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [*Caenorhabditis elegans*]//2.4e-50:302:90//Hs.19196:W74577  
 R-NT2RP2003751  
 R-NT2RP2003752  
 R-NT2RP2003753  
 R-NT2RP2003754//ESTs//6.2e-26:14:88//Hs.64036:AA12770  
 R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:AF047437

R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811  
 R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836  
 R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955  
 R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077  
 5 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838  
 R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124  
 R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167  
 R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341  
 R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611  
 10 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.75875:U49278  
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//Hs.35086:AB014458  
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:AB007916  
 15 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347  
 R-NT2RP2003984  
 R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087  
 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:AI149968  
 20 R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478  
 R-NT2RP2004041  
 R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706  
 R-nnnnnnnnnnnn//ESTs//1.4e-110:559:96//Hs.71916:AA219699  
 25 R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204  
 R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461  
 R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036  
 R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500  
 R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241  
 30 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e-118:583:97//Hs.16520:AI224533  
 R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544  
 R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974  
 R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589  
 35 R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167  
 R-NT2RP2004196  
 R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756  
 R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972  
 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499:98//Hs.143460:AA483305  
 40 R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116  
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530:93//Hs.54900:AF039687  
 R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483  
 45 R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744  
 R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187  
 R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056  
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544:96//Hs.61152:AF000416  
 50 R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788  
 R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223  
 R-NT2RP2004347  
 R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173  
 R-NT2RP2004365//ESTs//6.0e-101:511:99//Hs.38897:AI199316  
 R-NT2RP2004366//ESTs//1.0e-101:511:99//Hs.38897:AI199316  
 R-NT2RP2004373//ESTs//4.1e-101:511:99//Hs.38897:AI199316  
 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME II [Caenorhabditis elegans]//1.4e-11:108:82//Hs.30490:AA146916

R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646  
 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473  
 R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900  
 R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921  
 5 R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121  
 R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124  
 R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695  
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PKD1) mRNA, complete cds//  
 8.6e-34:143:98//Hs.154729:AF017995  
 10 R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700  
 R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320  
 R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081  
 R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347  
 R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470  
 15 R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661  
 R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126  
 R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666  
 R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862  
 R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-07:  
 20 149:76//Hs.12845:N28835  
 R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497  
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-116:567:96//Hs.5198:AJ006291  
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520:96//Hs.29956:  
 AB007929  
 25 R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930  
 R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858  
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600:96//Hs.154919:  
 AB014525  
 R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:AI149793  
 30 R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433  
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594:96//Hs.4236:  
 AB007947  
 R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015  
 R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423  
 35 R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774  
 R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013  
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//  
 8.0e-116:564:96//Hs.40820:AF058953  
 R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579  
 40 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:  
 AF054179  
 R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906  
 R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803  
 R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567  
 45 R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529  
 R-nnnnnnnnnnnn//ESTs//0.059:137:64//Hs.144109:AI345543  
 R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941  
 R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458  
 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087  
 50 R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496  
 R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910  
 R-NT2RP2004985  
 R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902  
 R-NT2RP2005000  
 R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235  
 R-nnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161  
 R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507  
 R-NT2RP2005031//ESTs//3.1e-79:379:99//Hs.139709:AA227887  
 R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220  
 5 R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757  
 R-NT2RP2005108  
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:AB014564  
 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.100555:X98743  
 10 R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383  
 R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180:AI341261  
 R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744  
 R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438  
 15 R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582  
 R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648  
 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513:95//Hs.155218:AJ007509  
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-115:577:96//Hs.7600:H98166  
 20 R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258  
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587  
 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503  
 25 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596  
 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272  
 R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001  
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219  
 30 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590  
 R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261  
 R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338  
 R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701  
 35 R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699  
 R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445  
 R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544  
 40 R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247  
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304  
 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697  
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631  
 45 R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068  
 R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423  
 R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096  
 R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307  
 50 R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936  
 R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019  
 R-NT2RP2005476//ESTs//5.1 e-40:205:9811Hs.101577:AI168526  
 R-NT2RP2005490//ESTs//L3e-70:364:96//Hs.134382:AA083573  
 R-NT2RP2005491//EST//0.012 220 60//Hs.144448 AA812455  
 R-NT2RP2005496//ESTs//5.1e-74 263 81//Hs.10279 AA757421  
 R-NT2RP2005498//ESTs, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:AI138993

R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755  
 R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME  
 I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071  
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:  
 5 570:9411Hs.119023:AF092563  
 R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:  
 433:95//Hs.36942:AA524535  
 R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856  
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:  
 10 AJ012449  
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:  
 AB007963  
 R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572  
 R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567  
 15 R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169  
 R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240  
 R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733  
 R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060  
 R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788  
 20 R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229  
 R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211  
 R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740  
 R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173  
 R-NT2RP2005651//ESTs, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:  
 25 AA868470  
 R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302  
 R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987  
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//  
 Hs.25664:AF089814  
 30 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229  
 R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236  
 R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643  
 R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tauros]//2.8e-68:376:93//Hs.  
 9095:AA532630  
 35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:  
 AB018342  
 R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98//  
 Hs.14298:AI417523  
 R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982  
 40 R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455  
 R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153  
 R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258  
 R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064  
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//  
 45 Hs.159651:AF068868  
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.  
 26285:AF082516  
 R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163  
 R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463  
 50 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-  
 112:559:96//Hs.14214:AI189379  
 R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.  
 22151:AI214321  
 R-NT2RP2005781//ESTs//1.7e-103:525:96//Hs.70589:AA868470  
 R-NT2RP2005784//ESTs//1.7e-103:525:96//Hs.70589:AA868470  
 R-NT2RP2005804//ESTs//8.8e-108:560:94//Hs.159597:AJ012449  
 R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746  
 R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122  
 R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403  
 R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062  
 R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462  
 5 R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105  
 R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133  
 R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315  
 R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268  
 R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:  
 10 94//Hs.16667:T92427  
 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170  
 R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419  
 R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988  
 R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080  
 15 R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347  
 R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II  
 [C.elegans]//1.2e-50:278:94//Hs.7194:AI185631  
 R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492  
 R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714  
 20 R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093  
 R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918  
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//  
 Hs.46440:U21943  
 R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365  
 25 R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522  
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258  
 R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435  
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:  
 AB014554  
 30 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276  
 R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398  
 R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484  
 R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312  
 R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253  
 35 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928  
 R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999  
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262  
 R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015  
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:  
 40 N78664  
 R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771  
 R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412  
 R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321  
 R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411  
 45 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:  
 77//Hs.1361:M55053  
 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.  
 115325:D84488  
 R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092  
 50 R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146  
 R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595  
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266  
 R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478  
 R-NT2RP2006472//ESTs//3.3e-90:473:95//Hs.29216:AA016670  
 R-NT2RP2006534//ESTs//1.1e-90:344:98//Hs.10210:AA52494  
 R-NT2RP2006554//ESTs//1.1e-90:460:95//Hs.47095:AA181474  
 R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886  
 R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

- R-nnnnnnnnnnn/ESTs//2.0e-112:533:98//Hs.18685:AI393829  
 R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112  
 R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598  
 5 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972  
 R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219  
 R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213  
 R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202  
 10 R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095  
 R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574  
 R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029  
 R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715  
 R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241  
 15 R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000  
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:AB011164  
 R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418  
 R-NT2RP3000186  
 20 R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882  
 R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091  
 R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306  
 R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817  
 R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819  
 25 R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239  
 R-NT2RP3000251  
 R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177  
 R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073  
 R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446  
 30 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:AI191323  
 R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117  
 R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438  
 R-NT2RP3000324  
 35 R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267  
 R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689  
 R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225  
 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177  
 R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741  
 40 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423  
 R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303  
 R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106  
 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185  
 45 R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947  
 R-NT2RP3000433  
 R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340  
 R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254  
 50 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102  
 R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492  
 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.114963:L34408  
 R-NT2RP3000481//ESTs//0.12:384:60//Hs.88684:AA88514  
 R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X1665  
 R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151  
 R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161



R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832  
 R-nnnnnnnnnnnn/DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325  
 R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]/3.2e-104:543:95//Hs.93796:  
 C06063  
 5 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575  
 R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878  
 R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779  
 R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180  
 R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166  
 10 R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188  
 R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761  
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305  
 R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]  
 //9.6e-113:552:97//Hs.23900:U82984  
 15 R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717  
 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266  
 R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460  
 R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139  
 R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963  
 20 R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196  
 R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399  
 R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]/2.8e-89:462:95//Hs.116793:AA779588  
 R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]/5.2e-82:466:91//Hs.66048:  
 AA524416  
 25 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631  
 R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997  
 R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135  
 R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857  
 R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965  
 30 R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651  
 R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332  
 R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691  
 R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571  
 R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989  
 35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:  
 U35234  
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:  
 AB007920  
 R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653  
 40 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798  
 R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090  
 R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778  
 R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]/5.7e-92:522:90//  
 Hs.96200:AA218942  
 45 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375  
 R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232  
 R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628  
 R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186  
 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898  
 50 R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817  
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158  
 R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692  
 R-nnnnnnnnnnnn/Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397  
 R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374  
 R-NT2RP3001433//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001434//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001435//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001436//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001437//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001438//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001439//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001440//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001441//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001442//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001443//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001444//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001445//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001446//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001447//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001448//ESTs//1.4e-104:541:94//Hs.73239:AA573761  
 R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994  
 R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA644658  
 R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280  
 R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009  
 R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783  
 5 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395  
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//  
 6.8e-112:549:9711Hs.28285:AF064801  
 R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047  
 R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750  
 10 R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463  
 R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:  
 AA524416  
 R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477  
 R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337  
 15 R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194  
 R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328  
 R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798  
 R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598  
 R-NT2RP3001629  
 20 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149  
 R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989  
 R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709  
 R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030  
 R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189  
 25 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648  
 R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225  
 R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558  
 R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390  
 R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312  
 30 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618  
 R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669  
 R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]  
 //4.1e-80:444:91//Hs.6823:W18181  
 R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099  
 35 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923  
 R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810  
 R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440  
 R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968  
 R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:  
 40 N92517  
 R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725  
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:  
 AB007928  
 R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900  
 45 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962  
 R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292  
 R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117  
 R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900  
 R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792  
 50 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642  
 R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180  
 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666  
 R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:  
 AI123300  
 R-NT2RP3001931//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:  
 AI123300  
 R-NT2RP3001931//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:  
 AI123300  
 R-NT2RP3001938//ESTs, Highly similar to SPORULATION SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]  
 //1.3e-95:483:96//Hs.5771:W74591



- R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365  
 R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573  
 R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172  
 5 R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [*Drosophila melanogaster*]//5.9e-109:537:97//Hs.19348:AA151678  
 R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502  
 R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871  
 R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [*H.sapiens*]//5.0e-101:524:95//Hs.32580:AI123601  
 10 R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169  
 R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945  
 R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159  
 R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973  
 R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958  
 15 R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377  
 R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240  
 R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080  
 R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678  
 R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641  
 20 R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262  
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587  
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314  
 R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286  
 25 R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975  
 R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698  
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:AB007961  
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [*Saccharomyces cerevisiae*]//112.0e-56:387:86//Hs.144597:W20143  
 30 R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850  
 R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116  
 R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553  
 R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423  
 35 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [*Mus musculus*]//3.0e-100:528:94//Hs.90353:N98551  
 R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355  
 R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912  
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [*C.elegans*]//5.9e-83:392:99//Hs.101364:AA534439  
 40 R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809  
 R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466  
 R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441  
 R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520  
 R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982  
 45 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [*Mus musculus*]//3.3e-107:535:96//Hs.27437:AA004208  
 R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632  
 R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774  
 R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007  
 50 R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226  
 R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944  
 R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796  
 R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634  
 R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573  
 R-NT2RP3003230//ESTs, Highly similar to TROPONIN 1 [Dictyostelium]//1.0e-100:528:94//Hs.90353:N98551  
 55 R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343

- R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628  
 R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960  
 R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061  
 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983  
 5 R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035  
 R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055  
 R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818  
 R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261  
 R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931  
 10 R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445  
 R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289  
 R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993  
 R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102  
 R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155  
 15 R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567  
 R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272  
 R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721  
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418:67//Hs.139488:AI124095  
 20 R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372  
 R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041  
 R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023  
 R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156  
 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:AF004828  
 25 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:AB018268  
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549:94//Hs.7886:AI057529  
 30 R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556  
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA//4.1e-33:217:88//Hs.8068:U00952  
 R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430  
 R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681  
 35 R-NT2RP3003564  
 R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721  
 R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944  
 R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759  
 R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448  
 40 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//Hs.17217:U49957  
 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310  
 R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714  
 R-NT2RP3003672  
 R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036  
 45 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768  
 R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923  
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:AB018300  
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863  
 50 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747  
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913  
 R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754  
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9410:W72446  
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627  
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761

R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]/9.6e-98:511:95//Hs.26955:AI333224  
 R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743  
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611  
 5 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888  
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298  
 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170  
 R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726  
 10 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933  
 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221  
 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409  
 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593  
 R-NT2RP3 004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142  
 15 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714  
 R-NT2RP3004041  
 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820  
 R-NT2RP3004070//ESTs//5.5e-108:552:9511Hs.23392:AI310139  
 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W4537  
 20 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104  
 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045  
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]/3.5e-76:402:95//Hs.55847:W31092  
 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696  
 25 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334  
 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425  
 R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093  
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]/1.8e-40:200:100//Hs.26089:AA195126  
 30 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]/1.1e-41:266:89//Hs.6314:AA522619  
 R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]/3.7e-112:547:97//Hs.99819:AI346680  
 R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794  
 R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252  
 35 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827  
 R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628  
 R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]/1.6e-89:468:95//Hs.5117:AA831530  
 R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623  
 40 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630  
 R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264  
 R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258  
 R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223  
 R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044  
 45 R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224  
 R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]/0.30:253:58//Hs.97184:AA385934  
 R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985  
 R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621  
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917  
 50 R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616  
 R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332  
 R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406  
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.9e-107:501:97//Hs.5003:AB007917  
 R-NT2RP3004480//ESTs//1.1e-104:485:95//Hs.106371:W42501  
 R-NT2RP3004498//ESTs, Moderately similar to ORF2, function unknown, [H.sapiens]/3.4e-100:508:95//Hs.47393:AA218858

R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735  
R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//  
1.8e-83:465:92//Hs.137064:AA318257  
R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971  
5 R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865  
R-nnnnnnnnnnnnn  
R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232  
R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461  
R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674  
10 R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493  
R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456  
R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213  
R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157  
R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723  
15 R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase  
(GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680  
R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335  
R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560  
R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219  
20 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266  
R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:AI345945  
R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030  
R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287  
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538  
25 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:  
AB007952  
R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014  
R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294  
R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III  
30 [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436  
R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295  
R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569  
R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257  
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:  
35 AB014600  
R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788  
R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390  
R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185  
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354:96//Hs.155481:  
40 AJ006470  
R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757  
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:  
AF091092  
R-NT2RP4000263  
45 R-nnnnnnnnnnnnn/ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]  
//4.7e-104:525:96//Hs.152069:AA548972  
R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631  
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524  
R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760  
50 R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390  
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:  
AB018281  
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-  
107:398:99:398:99//Hs.10488:AB014680  
R-NT2RP4000370//ESTs//8.8e-61:355:98//Hs.10488:AB014680  
R-NT2RP4000376//ESTs//5.8e-99:465:99//Hs.27182:AA604494  
R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376  
R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:

91//Hs.26156:AA630975

R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTER-GENIC REGION [*Saccharomyces cerevisiae*]/8.9e-95:468:96//Hs.93871:AI191318

R-NT2RP4000424//ESTs/3.7e-98:473:98//Hs.24945:AI189011

5 R-NT2RP4000448//ESTs/2.6e-79:446:91//Hs.25159:R60955

R-NT2RP4000449//ESTs/3.6e-98:468:98//Hs.31176:AI037953

R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783

R-NT2RP4000480//ESTs/4.5e-89:455:96//Hs.62638:AA127740

10 R-NT2RP4000480//ESTs/4.9e-92:431:99//Hs.121072:AI204167

R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [*C.elegans*]/1.2e-40:125:97//Hs.56124:AI424792

R-NT2RP4000515//EST/6.7e-30:183:90//Hs.150710:AI122713

15 R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868

R-NT2RP4000518//EST/0.091:178:58//Hs.133031:AI049874

R-NT2RP4000519

R-NT2RP4000524//ESTS, Highly similar to rsec8 [*R.norvegicus*]/3.4e-93:496:93//Hs.107394:H07126

R-NT2RP4000528//EST/0.84:130:66//Hs.140208:AA702213

20 R-NT2RP4000541//EST/5.2e-63:337:94//Hs.156337:AI337328

R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [*R.norvegicus*]/8.2e-92:448:98//Hs.25597:H93026

R-NT2RP4000588//ESTs/3.8e-94:445:98//Hs.44077:N28840

R-NT2RP4000614//ESTs/6.5e-18:159:83//Hs.24549:N57263

25 R-NT2RP4000638//ESTs/2.5e-46:296:87//Hs.132722:AA618531

R-NT2RP4000648//ESTs/2.6e-103:559:93//Hs.23794:W80393

R-NT2RP4000657//ESTs/1.0:189:60//Hs.87073:AA972704

R-NT2RP4000704//ESTs/2.8e-101:509:96//Hs.84824:AA935651

R-NT2RP4000724//ESTS/1.5e-83:442:94//Hs.142114:AA205615

30 R-NT2RP4000728//ESTs/0.84:61:75//Hs.145334:AI251399

R-NT2RP4000739//ESTs/8.8e-80:418:94//Hs.42959:N21211

R-NT2RP4000781//ESTs/1.4e-79:376:99//Hs.135458:AI081312

R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:94//Hs.25132:AB007939

35 R-NT2RP4000833//ESTs/5.8e-46:309:85//Hs.163979:AA828834

R-NT2RP4000837//ESTs/1.7e-112:539:97//Hs.97718:AI334028

R-NT2RP4000855//ESTs/1.1e-95:486:95//Hs.5345:AA988104

R-NT2RP4000865//EST/6.2e-68:412:89//Hs.142196:AA258356

R-NT2RP4000878//ESTs/1.9e-80:417:95//Hs.104716:AI023185

40 R-NT2RP4000879//ESTs/1.8e-42:211:99//Hs.89991:AI374617

R-NT2RP4000896//ESTs/1.2e-89:453:97//Hs.100182:N92594

R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [*H.sapiens*]/5.9e-17:134:85//Hs.14146:W92235

R-NT2RP4000928//ESTs/4.3e-14:84:100//Hs.155360:AA984683

45 R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95//Hs.24812:AF069532

R-NT2RP4000929//ESTs/1.3e-119:567:98//Hs.62717:AA044905

R-NT2RP4000955//ESTs/3.5e-10:119:78//Hs.42946:N21111

R-NT2RP4000973//ESTs/2.8e-05:93:69//Hs.155126:AA563986

50 R-NT2RP4000975//ESTs/4.4e-58:324:95//Hs.126070:AA045179

R-NT2RP4000979//ESTs/3.5e-42:468:73//Hs.106210:AI193017

R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98//Hs.12457:AF052123

R-NT2RP4000989//ESTs/1.3e-122:581:98//Hs.10499:AA528018

R-NT2RP4000996//ESTs/9.2e-113:579:94//Hs.23762:N26620

R-NT2RP4001004//ESTs/3.6e-78:389:98//Hs.156290:AI016769

R-NT2RP4001006//ESTS, Moderately similar to ORF2: function unknown [*H.sapiens*]/6.6e-124:574:99//Hs.

47393:AA218858

R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI418635

R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI336292

R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//3.6e-114:569:96//Hs.6762:AA088424

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94//Hs.100955:AB007859

R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]//2.1e-103:485:99//Hs.10114:AD45945

R-NT2RP4001078

R-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial//1.7e-119:569:98//Hs.106778:AJ010953

R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668

R-ntntntntntntntntntnt/Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164

R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:AI344055

R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617

R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737

R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357

R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476

R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890

R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//5.4e-113:573:96//Hs.5249:U55977

R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453

R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171

R-NT2RP4001150//ESTs//1.9e-90:422:100//Hs.125490:AI138884

R-NT2RP4001159

R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278

R-ntntntntntntntntntnt/ESTs//1.1 e-25:140:97//Hs.83756:AI002822

R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514

R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495

R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//4.4e-123:624:95//Hs.22744:AI379892

R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750

R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103

R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120

R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255

R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430

R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933

R-ntntntntntntntntntnt/ESTs//2.9e-34:213:91//Hs.43100:AA186588

R-NT2RP4001313

R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892

R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612

R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732

R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837

R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616

R-NT2RP4001372

R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]//1.7e-108:546:96//Hs.32271:AA203680

R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299

R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501

R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.8e-79:438:93//Hs.21938:W81045

R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132

R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649

R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [H.sapiens]//1.6e-102:498:97//Hs.62386:AA512948

R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339422

R-NT2RP4001455

R-NT2RP4001470

R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655

R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846

R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511  
R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385  
R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:A1377863  
R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:A1336292  
R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928  
R-nnnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:88//Hs.136189:AA133224  
R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552  
R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285  
R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437  
R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251  
R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906  
R-NT2RP4001575  
R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]//8.7e-112:557:97//Hs.7558:AA526812  
R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776  
R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657  
R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737  
R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:AF007151  
R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361  
R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734  
R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805  
R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.15562:U96629  
R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941  
R-nnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-CURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:A1141922  
R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692  
R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926  
R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315  
R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:W28098  
R-NT2RP4001803  
R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:A1161133  
R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:A1218434  
R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826  
R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663  
R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210  
R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087  
R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602  
R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:A1345528  
R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:A1018606  
R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:A1417099  
R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848  
R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436  
R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:A1341793  
R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73919:X81637  
R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457:94//Hs.41793:AA775879  
R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252  
R-NT2RP4002018

NT2RP4002019  
56/Hs.4111:AA588154  
R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738  
R-NT2HP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106

R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679  
 R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198  
 R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507  
 5 R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565  
 R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407  
 R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592  
 R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555  
 10 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272  
 R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090  
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934  
 15 R-OVARC1000004  
 R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929  
 R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635  
 R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273  
 R-OVARC1000017  
 20 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286  
 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073  
 R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041  
 R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367  
 R-OVARC1000071//ESTs//2.5e-60:321:96//Hs.25010:R6787  
 25 R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259  
 R-nnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703  
 R-OVARC1000091//ESTs, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596:94//Hs.20597:W58370  
 R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942  
 30 R-OVARC1000106  
 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250  
 R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312  
 R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482  
 35 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214  
 R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090  
 R-OVARC1000151  
 R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023  
 R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629  
 40 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258  
 R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864  
 R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874  
 R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958  
 45 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130  
 R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079  
 R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476  
 R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777  
 50 R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449  
 R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743  
 R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682  
 R-OVARC1000347//EST//0.0014:145:65//Hs.136945:AA76567  
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423  
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928

- R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219  
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670  
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237  
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034  
 5 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426  
 R-OVARC1000437  
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671  
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//  
 Hs.73614:U83460  
 10 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:  
 AB014583  
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582  
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576  
 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211  
 15 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926  
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947  
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983  
 R-OVARC1000496  
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484  
 20 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:AF088219  
 R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248  
 R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021  
 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106  
 R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285  
 25 R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587  
 R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627  
 R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219  
 R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053  
 R-OVARC1000605  
 30 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.  
 159897:AB007970  
 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073  
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:  
 AB011162  
 35 R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480  
 R-nnnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522  
 R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875  
 R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517  
 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901  
 40 R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461  
 R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:  
 AI141736  
 R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918  
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-  
 45 28:430:69//Hs.42457:AA523306  
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016  
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793  
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659  
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066  
 50 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764  
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:  
 Y17711  
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637  
 R-OVARC1000850//H.sapiens PR39 mRNA, complete cds//1.1e-31:100:64//Hs.108447:AJ000517  
 R-OVARC1000862//EST//4.9e-44:288:81//Hs.150663:AA923091  
 R-OVARC1000876//ESTs//1.0e-15:573:96//Hs.87287:AI150674  
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292  
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC

REGION [Bacillus subtilis]/7.9e-98:525:93//Hs.10366:W21953  
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777  
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401  
 R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350  
 5 R-OVARC1000912  
 R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814  
 R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127  
 R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696  
 R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215  
 10 R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794  
 R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971  
 R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219  
 R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394  
 R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909  
 15 R-OVARC1000984//ESTs, Weakly similar to No definition line found [C.elegans]/3.5e-68:346:96//Hs.25544:AA532784  
 R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811  
 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874  
 R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448  
 20 R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:77//Hs.139107:K00629  
 R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270  
 R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117  
 R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630  
 R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:  
 25 137:74//Hs.77579:AF013263  
 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149  
 R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046  
 R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384  
 R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962  
 30 R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231  
 R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652  
 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:AF082657  
 R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844  
 35 R-OVARC1001074  
 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029  
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897  
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:AF051782  
 40 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.46468:U45984  
 R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548  
 R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312  
 45 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]/2.2e-66:346:95//Hs.53263:AA173226  
 R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223  
 R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727  
 R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200  
 50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219  
 R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223  
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:80//Hs.97203:U83171  
 R-OVARC1001188//EST//1.5e-24:66:69//Hs.136137:AA08891  
 R-OVARC1001195//EST//1.1e-24:66:69//Hs.136137:AA08891  
 R-OVARC1001232//ESTs//0.2e-05:358:91//Hs.6449:W95020  
 R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668  
 R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

- R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166  
 R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929  
 R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708  
 R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532  
 5 R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113  
 R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885  
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763:AB011090  
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73919:X81637  
 10 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344  
 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219  
 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356  
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247  
 15 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216  
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657  
 R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844  
 R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777  
 R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415  
 20 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468:AB011147  
 R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958  
 R-OVARC1001391  
 R-nnnnnnnnnnnnn//ESTs//0.003 9:48:95//Hs.117964:N20913  
 25 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651  
 R-OVARC1001419  
 R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136  
 R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427  
 R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345  
 30 R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592  
 R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700  
 R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694  
 R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089  
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534:AF016507  
 35 R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219  
 R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539  
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492  
 R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388  
 40 R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//4.4e-20:150:89//Hs.155160:AF031166  
 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087  
 R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019  
 R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965  
 45 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869  
 R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659  
 R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854  
 R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080  
 R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784  
 50 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485:AA046954  
 R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276  
 R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563:AF057280  
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.1e-109:567:94//Hs.155377:U97670

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:AB014575

R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127

R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604

5 R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978

R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333

R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688

R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831

R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110

10 R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705

R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621

R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160

R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809

R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-105:571:91//Hs.25300:AF070611

15 R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476

R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:AB011147

R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310

20 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749

R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435

R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855

R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842

25 R-OVARC1001928

R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456

R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637

R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:AI379892

30 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875

R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729

R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887

R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531

35 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934

R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556

R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315

40 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860

R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130

R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691

R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825

45 R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923

R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631

R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160

R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478

50 R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337

R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920

R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557

R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223

R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870

R-PLACE1000048//Human L1 repeat mRNA with 2 open reading frames//1.1e-10:100:100//Hs.109268:AF070557

R-PLACE1000050//ESTs//9.7e-90:453:96//Hs.27410:N25612

R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

R-PLACE1000066//ESTs, Weakly similar to coded for by *C. elegans* cDNA yk10c10.3 [*C.elegans*]/1.4e-61:331:94//Hs.30026:AI356771  
R-PLACE1000078//ESTs/2.6e-30:212:85//Hs.89312:AA167659  
R-PLACE1000081  
5 R-PLACE1000094  
R-PLACE1000133//ESTs/4.4e-87:448:94//Hs.93748:AA884505  
R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [*H.sapiens*]/5.5e-103:538:94//Hs.9670:AA632135  
R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds/4.1e-114:594:94//Hs.151017:AF058291  
10 R-PLACE1000185//ESTs, Weakly similar to No definition line found [*C.elegans*]/2.0e-19:114:95//Hs.7036:W22072  
R-PLACE1000213//ESTs/9.4e-99:494:96//Hs.24398:AI262946  
R-PLACE1000214//ESTs/5.3e-98:466:98//Hs.28661:AA805916  
15 R-PLACE1000236//Human BENE mRNA, partial cds/1.7e-19:162:84//Hs.85889:U17077  
R-PLACE1000246//EST/0.026:134:66//Hs.135611:Z21545  
R-PLACE1000292//ESTs/2.5e-80:418:96//Hs.138233:N57912  
R-PLACE1000332//EST/1.7e-82:422:96//Hs.118637:T61940  
R-PLACE1000347//ESTs/8.5e-36:180:100//Hs.6377:AA632424  
20 R-PLACE1000374//ESTs/2.8e-90:434:98//Hs.161785:AI423126  
R-PLACE1000380//ESTs/1.0e-81:399:97//Hs.47105:AI334994  
R-PLACE1000383//ESTs/3.7e-75:405:94//Hs.23200:AA203708  
R-PLACE1000401//ESTs/1.4e-16:212:72//Hs.151665:AA020959  
R-PLACE1000406//ESTs/2.1e-51:259:97//Hs.129651:N53089  
25 R-PLACE1000420//ESTs/7.7e-92:471:95//Hs.144407:AA737799  
R-PLACE1000421//ESTs/2.9e-14:282:67//Hs.142068:AA176125  
R-PLACE1000424//EST/2.9e-35:453:70//Hs.162404:AA573131  
R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds/1.6e-47:472:77//Hs.113259:AF023456  
30 R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [*H.sapiens*]/2.0e-58:410:81//Hs.97579:AA398118  
R-PLACE1000453//ESTs/2.3e-85:442:95//Hs.9725:AA039793  
R-PLACE1000481//ESTs, Weakly similar to Ndr protein kinase [*H.sapiens*]/3.2e-109:549:95//Hs.19074:U69566  
R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [*R.norvegicus*]/3.5e-83:435:94//Hs.26510:AA700425  
35 R-PLACE1000540//ESTs/3.2e-58:281:99//Hs.118270:AA844729  
R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds/2.2e-32:208:88//Hs.153026:AB014540  
R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC REGION [*Saccharomyces cerevisiae*]/1.9e-26:220:81//Hs.163791:W25348  
40 R-PLACE1000564//ESTs/1.1e-54:302:92//Hs.158520:AI380485  
R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds/5.5e-43:404:75//Hs.153014:AB002353  
R-nnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD/6.1e-79:542:82//Hs.62661:M55542  
R-PLACE1000596//ESTs/0.0028:364:59//Hs.106090:AA457030  
45 R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds/4.3e-49:295:90//Hs.154326:D42087  
R-PLACE1000610//ESTs/0.0010:104:74//Hs.17413:N45301  
R-PLACE1000636//ESTs/1.8e-64:340:95//Hs.100895:AA479308  
R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds/5.3e-101:506:96//Hs.5819:AF102265  
50 R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))/1.4e-102:559:92//Hs.29595:AJ005896  
R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds/2.8e-10:281:64//Hs.128763:AF009353  
R-PLACE1000712//ESTs/7.8e-60:317:95//Hs.8245:AA115485  
R-PLACE1000714//ESTs/1.4e-60:317:95//Hs.8245:AA115485  
R-PLACE1000749//EST/0.013:186:61//Hs.135443:AI077396  
R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [*C. el-*

egans]/3.9e-40:224:94//Hs.87889:AA262008

R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548

5 R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482

R-nnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219

R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189

R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:220:86//Hs.117576:R33135

10 R-nnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588

R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039

R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118:-AI141558

R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846

15 R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091

R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697

R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941

R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689

R-PLACE1000979

20 R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725

R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:343:93//Hs.5662:AA868361

R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146

R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878

R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736

25 R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762

R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120

R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124

R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580

R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141

30 R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268

R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610

R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594

R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834

R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.115211:AA287527

35 R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297

R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//1.9e-99:512:94//Hs.24884:AA176812

R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464

40 R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131

R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371

R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780

R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460

R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus]//2.7e-22:181:84//Hs.48320:AA149548

45 R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:W27601

R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056

50 R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//Hs.50984:U01160

R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077

R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF096615

R-PLACE1001387//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536

R-PLACE1001384//Homo sapiens clone 24566 domain protein MCH-10/MCH-10 mRNA, complete cds//1.4e-45:94//Hs.21301:AF093419

R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280

R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555  
 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348  
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:AF091087  
 5 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800  
 R-PLACE1001440  
 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.  
 R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547  
 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625  
 10 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617  
 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361  
 R-PLACE1001517//Homo sapiens hGAAI mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969  
 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153  
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:  
 15 170:85//Hs.155456:AA707265  
 R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431  
 R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249  
 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601  
 R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904  
 20 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683  
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174  
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.114547:AA167095  
 25 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526  
 R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640  
 R-PLACE10016727//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804  
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250  
 30 R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124  
 R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903  
 R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667  
 R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993  
 35 R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171  
 R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113  
 R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266  
 R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479  
 R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937  
 40 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243  
 R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662  
 R-PLACE1001761  
 R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980  
 45 R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236  
 R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//1.3e-93:463:95//Hs.40820:AF058953  
 R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219  
 50 R-PLACE1001845  
 R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868  
 R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009  
 R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098  
 R-PLACE1001920//Homo sapiens TNF-induced protein G2.1 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174  
 R-PLACE1001921//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001922//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001923//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001924//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001925//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001926//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001927//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001928//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001929//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001930//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001931//ESTs//0.00039:126:65//Hs.123267:AA807352  
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 R-PLACE1001941//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001942//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001943//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001944//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001945//ESTs//0.00039:126:65//Hs.123267:AA807352  
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 R-PLACE1001947//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001948//ESTs//0.00039:126:65//Hs.123267:AA807352  
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 R-PLACE1001954//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001955//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001956//ESTs//0.00039:126:65//Hs.123267:AA807352  
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 R-PLACE1001961//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001962//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001963//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001964//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001965//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001966//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001967//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001968//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001969//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001970//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001971//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001972//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001973//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001974//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001975//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001976//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001977//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001978//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001979//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001980//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001981//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001982//ESTs//0.00039:126:65//Hs.123267:AA807352  
 R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941  
 R-PLACE1002046  
 R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595  
 R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094  
 5 R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619  
 R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552  
 R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632  
 R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311  
 R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293  
 10 R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937  
 R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614  
 R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189  
 R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965  
 15 R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745  
 R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793  
 R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788  
 R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892  
 R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257  
 20 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503  
 R-PLACE1002319//ESTs//1.4e-28:17 8:92//Hs.7353:AA209308  
 R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271  
 R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291  
 R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381  
 25 R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959  
 R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110  
 R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804  
 R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333  
 R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320  
 30 R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263  
 R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132  
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273  
 R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429  
 35 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869  
 R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609  
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256  
 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:93//Hs.99348:AC004774  
 40 R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491  
 R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437  
 R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131  
 R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738  
 45 R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778  
 R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208  
 R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147  
 R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749  
 50 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130  
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180  
 R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830  
 R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor[H.sapiens]//6.8e-75:445:90//Hs.14660:R14660  
 R-PLACE1002738//ESTs//1.7e-49:362:82//Hs.141254:AI334099  
 R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014

R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593  
 R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955  
 R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392  
 R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916  
 5 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094  
 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142  
 R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756  
 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539  
 10 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762  
 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332  
 R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995  
 R-PLACE1002962  
 R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202  
 15 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941  
 R-PLACE10029937//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268  
 R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268  
 R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499  
 20 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075  
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840  
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777  
 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.6318:AI131178  
 25 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359  
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920  
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757  
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467  
 30 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924  
 R-PLACE1003176  
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453  
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017  
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802  
 35 R-PLACE1003238//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123  
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460  
 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131  
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326  
 40 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986  
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993  
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:97//Hs.155050:AA908765  
 45 R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438  
 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701  
 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715  
 50 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636  
 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234  
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591  
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941  
 R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909  
 55 R-PLACE1003383//ESTs//0.0084:177:64//Hs.159695:AI37774  
 R-PLACE1003385//ESTs//0.0071:120:58//Hs.132187:AI039021  
 R-PLACE1003420//ESTs//0.0045:461:84//Hs.122565:AI126840  
 R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671  
 R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270  
 R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952  
 R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505  
 5 R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980  
 R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461  
 R-PLACE1003537//ESTs, Weakly similar to multispinning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.110439:N93209  
 R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321  
 10 R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591  
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956  
 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:R86178  
 15 R-PLACE1003584  
 R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542  
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AD77106  
 R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875  
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:D83200  
 20 R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299  
 R-aaaaaaaaaaaaa//ESTs//1.0:78:71//Hs.101248:T26446  
 R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943  
 R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285  
 R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247  
 25 R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607  
 R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521  
 R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866  
 R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639  
 R-PLACE1003723//ESTs//1.7e-89:448:96//Hs.157222:AA766987  
 30 R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087  
 R-PLACE1003760//Human globin gene//L9e-98:538:91//Hs.100090:M69023  
 R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512  
 R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965  
 R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798  
 35 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757  
 R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909  
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:AB011147  
 R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092  
 40 R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059  
 R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058  
 R-aaaaaaaaaaaaa  
 R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871  
 45 R-aaaaaaaaaaaaa  
 R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595  
 R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915  
 R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259  
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:AA100804  
 50 R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760  
 R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236  
 R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110  
 R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567  
 R-PLACE1003968//ESTs//1.1e-11:112:112//Hs.13851:AA111111  
 R-PLACE1004044//ESTs//1.3e-46:254:94//Hs.96802:AA44320  
 R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052  
 R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770

R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244  
R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714  
R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080  
R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601  
R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//4.7e-78:434:91//Hs.153504:AF044321  
R-PLACE1004197  
R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.5e-105:501:98//Hs.24640:AF069493  
R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952  
R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630  
R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209  
R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:100124  
R-PLACE1004270//ESTS//0.011:264:59//Hs.110044:AA181800  
R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:121:66//Hs.1938:S82362  
R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//1.4e-107:581:91//Hs.127007:AF084830  
R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114  
R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:279:77//Hs.38687:AA744496  
R-PI ACF1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.71435:AI253099  
R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588  
R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:77//Hs.1361:M55053  
R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:379:93//Hs.16232:AF100153  
R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309  
R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556  
R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-98:572:90//Hs.14202:N46000  
R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467  
R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665  
R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283  
R-PLACE1004451  
R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980  
R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721  
R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578  
R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194  
R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:278:61//Hs.89663:L13286  
R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117  
R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493  
R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164  
R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553  
R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.115325:084488  
R-PLACE1004550  
R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742  
R-PLACE1004629//ESTs, Weakly similar to OS-9 precursor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181  
R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903  
R-PLACE1004658//ESTs//1.4e-64:344:96//Hs.23508:AA101111  
R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254  
R-PLACE1004673//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004674//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004675//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004676//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004677//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004678//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004679//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004680//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004681//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004682//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004683//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004684//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004685//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004686//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004687//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004688//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004689//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004690//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004691//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004692//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004693//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004694//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004695//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004696//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004697//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004698//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004699//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004700//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004701//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004702//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004703//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004704//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004705//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004706//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004707//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004708//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004709//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004710//ESTs//1.0e-07:114:78//Hs.140225:AA704101  
R-PLACE1004711//ESTs//1.0e-07:114:78//Hs

- R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8e-90:510:91//Hs.80019:AF035606
- R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482
- R-PLACE1004686
- 5 R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552
- R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374
- R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]//3.4e-80:413:94//Hs.23528:AI279571
- R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997
- 10 R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N6391
- R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619
- R-nnnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195
- R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374
- R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367
- 15 R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548
- R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619
- R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178
- R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856
- R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250
- 20 R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356
- R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.73821:M35663
- R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185
- 25 R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299
- R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901
- R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]//6.5e-71:381:93//Hs.8383:AA013272
- R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308
- 30 R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456
- R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI211881
- R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597
- R-nnnnnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:AI221563
- 35 R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI424948
- R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.17839:AF099936
- R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980
- R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702166
- 40 R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013
- R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106
- R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789
- R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI291776
- R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335
- 45 R-PLACE1005026
- R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145:66//Hs.11215:N56719
- R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:AB011147
- 50 R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543:95//Hs.18625:AI074605
- R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103
- R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985
- R-PLACE1005085//Homo sapiens PYRIN (MEEV) mRNA, complete cds//1.0e-101:511:91//Hs.100086:AF035606
- R-PLACE1005086//ESTs//1.4e-115:126:AA584366
- R-PLACE1005101//Homo sapiens clone zap128 mRNA, complete cds//1.0e-101:511:91//Hs.75437:U4046
- R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336
- R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:

U91985

R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225

R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423

R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349

5 R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013

R-nnnnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA454227

R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589

R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830

R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211

10 R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532

R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767

R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524

R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633

R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516

15 R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322

R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937

R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797

R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614

R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960

20 R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343

R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975

R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901

R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394

R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978

25 R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304

R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423

R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503

R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607

R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046

30 R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875

R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220

R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:

AF071185

R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325

35 R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:

AJ006470

R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325

R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III

[Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927

40 R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555

R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR

[Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261

R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835

R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612

45 R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023

R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927

R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857

R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964

R-PLACE1005630

50 R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452

R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:

AF083255

R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169

R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//

55 3.3e-24:401:66//Hs.129727:AF035581

0098:129727:AF035581

R-PLACE1005707//EST//1.0e-63:106:63//Hs.125002:AA449332

R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259

R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]/1.3e-42:236:94//Hs.23889:AI341137

R-PLACE1005755//ESTs/2.8e-32:308:80//Hs.159821:AA524070

R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds/3.3e-47:268:87//Hs.154326:D42087

5 R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]/7.7e-15:88:98//Hs.109857:AA088385

R-PLACE1005802//ESTs/2.8e-19:208:76//Hs.9271:W30941

R-PLACE1005803//ESTs/2.6e-75:417:92//Hs.71414:AA131327

R-PLACE1005804//EST/6.5e-20:182:70//Hs.149844:AI287693

10 R-PLACE1005828//ESTs/3.0e-15:194:77//Hs.106236:N50058

R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)/0.040:435:58//Hs.75770:L41870

R-PLACE1005845//EST/5.0e-61:294:99//Hs.133202:AI050965

R-PLACE1005850//ESTs/3.4e-82:425:96//Hs.7966:AI203471

R-PLACE1005851//ESTs/2.9e-21:165:84//Hs.23607:N98305

15 R-PLACE1005876//ESTs/0.48:296:57//Hs.39140:AI041842

R-PLACE1005884//ESTs/0.0027:177:66//Hs.150295:AA570558

R-PLACE1005898//ESTs/1.7e-98:467:98//Hs.159475:AI339981

R-PLACE1005921//ESTs/5.8e-96:480:95//Hs.30822:AA885501

R-PLACE1005923//ESTs/1.8e-66:333:96//Hs.150890:AI341793

20 R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames/2.8e-27:382:70//Hs.23094:M19503

R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]/1.1e-70:377:93//Hs.5662:AA868361

R-PLACE1005934//ESTs/1.0e-42:251:91//Hs.25092:AA922142

R-PLACE1005936//ESTs/1.2e-88:461:94//Hs.94125:N62913

R-PLACE1005951//ESTs/1.4e-83:533:86//Hs.21148:AI183729

25 R-PLACE1005953

R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]/2.2e-83:494:88//Hs.108117:AI097079

R-PLACE1005966//ESTs/1.1e-95:465:97//Hs.98510:AI016239

R-PLACE1005968//EST/0.26:103:66//Hs.161300:AI420897

30 R-PLACE1005990

R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds/2.0e-45:481:74//Hs.153014:AB002353

R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]/3.1e-112:593:93//Hs.111449:AI192946

R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]/5.7e-100:596:88//Hs.24284:AA595596

35 R-PLACE1006017//ESTs/4.2e-18:296:68//Hs.133350:AI056276

R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]/4.1e-102:491:98//Hs.61164:AI096332

R-PLACE1006040//ESTs/1.2e-92:443:98//Hs.111680:N93765

R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/2.0e-26:213:77//Hs.139007:H74314

40 R-PLACE1006119//ESTs/0.14:257:61//Hs.113149:AA908904

R-PLACE1006129//ESTs/3.8e-54:285:97//Hs.18827:W68002

R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]/2.6e-99:560:91//Hs.5249:U55977

45 R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)/0.038:463:59//Hs.904:U84010

R-PLACE1006157//ESTs/0.014:341:58//Hs.121773:AI357886

R-PLACE1006159//EST/0.00036:247:61//Hs.140054:AA668925

R-PLACE1006164//ESTs/2.6e-31:362:73//Hs.141024:H07128

50 R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149/5.8e-54:286:94//Hs.152894:AC005239

R-nnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]/2.7e-79:393:96//Hs.19121:AI125280

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds/5.1e-118:597:95//Hs.30464:AF091433

R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/6.8e-24:244:94:195:16 A 3883

R-PLACE1006196//ESTs/0.106:382:90//Hs.8665:U9951

R-PLACE1006205//EST/1.7e-89:448:96//Hs.116665:AA669114

R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds/0.90:304:58//Hs.94986:U77664

R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI079555  
 R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472  
 R-nnnnnnnnnnnnn/Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142  
 R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.musculus]/1.3e-104:532:95//Hs.  
 41151:AI301961  
 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548  
 R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/1.6e-  
 07:321:62//Hs.53057:W67839  
 R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132  
 R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265  
 R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503  
 R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900  
 R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168  
 R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044  
 R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI079284  
 R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053  
 R-PLACE1006382  
 R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748  
 R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI281881  
 R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258  
 R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI278629  
 R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139  
 R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961  
 R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297  
 R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418  
 R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722  
 R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374  
 R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717  
 R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723  
 R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368  
 R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532  
 R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214  
 R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443  
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//  
 9.3e-118:590:95//Hs.155377:U97670  
 R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322  
 R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615  
 R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384  
 R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522  
 R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627  
 R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736  
 R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214  
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98//Hs.12472:AF038172  
 R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861  
 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622  
 R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658  
 R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234  
 R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515  
 R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335  
 R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989  
 R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847  
 R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159  
 R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]/  
 1.0e-87:481:92//Hs.141263:H64113  
 R-PLACE1006829//ESTs//1.1e-41:244:86//Hs.102319:AI246503  
 R-PLACE1006860//ESTs//0.8e-138:63//Hs.136649:AA-828354  
 R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35006  
 R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536

R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131  
 R-nnnnnnnnnnnr//ESTs//3.0e-95:496:94//Hs.47546:AA181348  
 R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089  
 R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168  
 5 R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514  
 R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078  
 R-nnnnnnnnnnnr//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956  
 R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520  
 R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:AI275982  
 10 R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636  
 R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257  
 R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366  
 R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971  
 R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503  
 15 R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575  
 R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027  
 R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202  
 R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646  
 R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417  
 20 R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948  
 R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794  
 R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765  
 R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998  
 R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619  
 25 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495  
 R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450  
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357:98//Hs.18272:N78499  
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909  
 30 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:AI275071  
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419  
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812  
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087  
 R-PLACE1007301  
 35 R-PLACE1007317  
 R-PLACE1007342  
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870  
 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488:96//Hs.24359:AA699594  
 40 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614  
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945  
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877  
 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771  
 45 R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.72165:AI243857  
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171  
 50 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514  
 R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230  
 R-PLACE1007478  
 R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975  
 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types) [H.sapiens]//1.5e-41:261:89//Hs.9029:W57657  
 R-PLACE1007507//ESTs//1.1e-48:457:94//Hs.129819:AA838366  
 R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657

- R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377  
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087  
 R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612  
 R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404  
 5 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840  
 R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257  
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179  
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:l61:65//Hs.76506:J02923  
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176  
 10 R-PLACE1007632  
 R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106  
 R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946  
 R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//  
 9.0e-37:190:97//Hs.23437:AA707331  
 15 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944  
 R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]  
 //3.4e-61:384:89//Hs.92918:AA133274  
 R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs.  
 91251:U66685  
 20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407  
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812:  
 AF061243  
 R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797:  
 AA476815  
 25 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619  
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121:  
 AB014585  
 R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322  
 R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778  
 30 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903  
 R-PLACE1007791//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//  
 8.6e-27:143:98//Hs.144194:AA706337  
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M 9503  
 R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044  
 35 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050  
 R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839  
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503  
 R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017  
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:  
 40 AB018309  
 R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178  
 R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832  
 R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060  
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.  
 45 92381:AB007956  
 R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510  
 R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966  
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.  
 5671:AF084530  
 50 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:  
 465:93//Hs.78106:AF079529  
 R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900  
 R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]  
 //3.8e-97:493:95//Hs.6141:U69564  
 R-PLACE1008000//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [H. norvegicus],  
 //2.0e-115:575:95//Hs.92395:AA779854  
 R-PLACE1008002//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [H. norvegicus],  
 //2.0e-115:575:95//Hs.92395:AA779854  
 R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [H. norvegicus],  
 //2.0e-115:575:95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935  
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269  
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469  
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334  
 5 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617  
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511  
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381  
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266  
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267  
 10 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107  
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102  
 R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701  
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871  
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990  
 15 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808  
 R-nnnnnnnnnnnnn  
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705  
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852  
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276  
 20 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//  
 Hs.146477:AI128445  
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656  
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579  
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052  
 25 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009  
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-  
 41:448:72//Hs.139007:H74314  
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242  
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:  
 30 536:87//Hs.7570:W31010  
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326  
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440  
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778  
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757  
 35 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562  
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928  
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761  
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387  
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636  
 40 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180  
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816  
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560  
 R-PLACE1008532  
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850  
 45 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223  
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064  
 R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:  
 AA778649  
 R-nnnnnnnnnnnnn  
 50 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454  
 R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972  
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512  
 R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612  
 R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002355  
 55 R-PLACE1008650//ESTs//1.1e-100:505:93//Hs.102401:AI004972  
 R-PLACE1008653//ESTs//1.1e-100:505:93//Hs.102401:AI004972  
 R-PLACE1008693//ESTs, Weakly similar to CYTOCHROME P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.8e-41:505:71//Hs.51048:X68830  
 R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

76//Hs.1361:M55053

R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600

R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303

5 R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408

R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313

R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930

R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217

10 R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905

R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490:93//Hs.110454:H11810

R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428

R-nnnnnnnnnnnnnnn

15 R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502

R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878

R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893

R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308

R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018

20 R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653

R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680

R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573

R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419

25 R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112

R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520

R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195

R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139

R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008

30 R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142

R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448

R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546

R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136

35 R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549

R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983

R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:AA703945

R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747

40 R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.93332:AA811920

R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005

R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322

R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948

45 R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707

R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717

R-PLACE10091867//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:Z78396

R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701

50 R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248

R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680

R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018

R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423

R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279

R-PLACE1009328//EST//1.1e-49:344:94//Hs.130558:AI004394

R-PLACE1009335//EST//1.1e-49:344:94//Hs.130558:AI004394

R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782

R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760

R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA161260  
 R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883  
 R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186  
 R-nnnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798  
 5 R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255  
 R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632  
 R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269  
 R-PLACE1099444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872  
 R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427  
 10 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:  
 AC004531  
 R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925  
 R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596  
 R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698  
 15 R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131  
 R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:  
 289:63//Hs.77579:AF013263  
 R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326  
 R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.  
 20 sapiens]//0.0012:56:91//Hs.12151:AA001818  
 R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:  
 AB014535  
 R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735  
 R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482  
 25 R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680  
 R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243338  
 R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858  
 R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701  
 R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213  
 30 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:  
 AB011159  
 R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483:79//Hs.140416:  
 AA778649  
 R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534  
 35 R-PLACE1009708//ESTs//3.0e-94:471:96//Hs.40091:N48582  
 R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529:92//Hs.3945:AA004210  
 R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489:89//Hs.  
 26194:AA033989  
 R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024  
 40 R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989  
 R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-  
 quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene  
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene  
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-  
 45 113:549:97//Hs.16411:AL030996  
 R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868  
 R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748  
 R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328  
 R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031  
 50 R-nnnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:  
 AI219740  
 R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563  
 R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276  
 R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI04317  
 R-PLACE1009935//ESTs//1.1e-61:113:70//Hs.131755:AA44961  
 R-PLACE1009947//Keratin 18//2.3e-61//Hs.2783:Z29074  
 R-PLACE1009967//ESTs//1.0e-67:424:98//Hs.13781:AI160540  
 R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347  
 R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219  
 R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:  
 AI141736  
 5 R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204  
 R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]//  
 7.6e-104:546:94//Hs.8215:AA521150  
 R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905  
 R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.  
 10 11183AF065482  
 R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375  
 R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424  
 R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615  
 R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:  
 15 U69567  
 R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015  
 R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103  
 R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270  
 R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130  
 20 R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359  
 R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897  
 R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313  
 R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466  
 R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037  
 25 R-PLACE1010231  
 R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478  
 R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545  
 R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535  
 R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788  
 30 R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081  
 R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568  
 R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219  
 R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.9e-  
 32:190:77//Hs.152369:AA504818  
 35 R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327  
 R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594  
 R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, partial//4.9e-35:166:86//Hs.53531:  
 AJ224162  
 R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152  
 40 R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816  
 R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:  
 AF039081  
 R-PLACE1010492  
 R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031  
 45 R-nnnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455  
 R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306  
 R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033  
 R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116  
 R-PLACE1010599  
 50 R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418  
 R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895  
 R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475  
 R-PLACE1010628//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:  
 391:95//Hs.163495:W57637  
 R-PLACE1010630//ESTs//4.5e-103:549:94//Hs.12783:AA731171  
 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102  
 R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:

91//Hs.22383:R51067

R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]/8.3e-103:538:94//Hs.105794:AA701659

R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973

R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:95//Hs.50758:AF092564

R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189

R-PLACE1010743

R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250

R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024

R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]/7.6e-111:575:94//Hs.10260:AI126627

R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558

R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:AI091203

R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896

R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472

R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048

R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]/1.4e-71:326:92//Hs.3385:N25917

R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182

R-PLACE1010891

R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983

R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023

R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630

R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093

R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126

R-nnnnnnnnnnnnn/Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:AF064244

R-PLACE1010944

R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519

R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219

R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]/1.0e-103:565:92//Hs.23259:AA532437

R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580

R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846

R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867

R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249

R-nnnnnnnnnnnnn/Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153

R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135

R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219

R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537

R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.6e-54:398:84//Hs.108740:W20094

R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478

R-PLACE1011111 4//ESTs//5.4e-90:475:94//Hs.69331:AA099587

R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]/3.0e-105:552:93//Hs.31257:AA875998

R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795

R-PLACE1011160//Homo sapiens mRNA for HRIHFB2038 partial cds//7.7e-97:534:91//Hs.28712:AB011133

R-PLACE1011166//ESTs, Weakly similar to HRIHFB2038 partial cds//1.1e-54:398:84//Hs.108740:W20094

R-PLACE1011167//ESTs, Weakly similar to HRIHFB2038 partial cds//1.1e-54:398:84//Hs.108740:W20094

R-PLACE1011178//ESTs

R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671  
R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299  
R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693  
R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602  
5 R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772  
R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913  
R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849  
R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807  
R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291  
10 R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578  
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A[Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337  
R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376  
R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194  
15 R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337  
R-nnnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102  
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607  
20 R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887  
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255  
R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278  
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294  
25 R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576  
R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421  
R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985  
R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672  
R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548  
30 R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067  
R-PLACE1011641//ESTs//2.5e-71:J38:100//Hs.153085:AA993965  
R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900  
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535  
R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036  
35 R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838  
R-PLACE1011675  
R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025  
R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410:83//Hs.23094:M19503  
40 R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392  
R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426  
R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative products}//7.3e-40:361:77//Hs.53217:Z48051  
R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K00627  
45 R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080  
R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179  
R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563  
R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067  
R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648  
50 R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913  
R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI275497  
R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268  
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617  
55 R-PLACE1011960//EST//1.3e-41:114:100//Hs.101365:R60578  
R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890

R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247  
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:AB018256  
 R-PLACE20000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069  
 5 R-PLACE20000007//ESTs//2.4e-110:564:95//Hs.65135:W89120  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:AF091080  
 R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211  
 R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504  
 10 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868  
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.154069:U06452  
 R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013  
 R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073  
 15 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622  
 R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652  
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:AB011147  
 20 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390  
 R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:AF027219  
 R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179  
 R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236  
 25 R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941  
 R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71//Hs.42400:AF022789  
 R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662  
 R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988  
 30 R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558  
 R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:AB011134  
 R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357  
 R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219  
 35 R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778  
 R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292  
 R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067  
 R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:AI382378  
 R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191  
 40 R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717  
 R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600  
 R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363  
 R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:AI004779  
 45 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664  
 R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:AI344055  
 R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380  
 R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058  
 50 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789  
 R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618  
 R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848  
 R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081  
 R-PLACE2000371//ESTs//8.6e-41:309:97//Hs.155138:AA158871  
 R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//8.8e-48:338:82//Hs.154150:U06452  
 R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781  
 R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189  
 R-PLACE2000399  
 R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA088424  
 5 R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941  
 R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739  
 R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333  
 R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEES142F [C.elegans]//3.0e-113:543:97//Hs.16933:AA976002  
 10 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523  
 R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986  
 R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887  
 R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390  
 R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714  
 15 R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638  
 R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228  
 R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642  
 R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838  
 R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:AB011147  
 20 R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763  
 R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979  
 R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830  
 R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727  
 25 R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739  
 R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792  
 R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369  
 R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142  
 R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815  
 30 R-PLACE3000155//ESTs//1.2e-19:192:79//Hs.131350:AA805223  
 R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//Hs.31532:H18272  
 R-PLACE3000157  
 R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219  
 35 R-PLACE3000160  
 R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798  
 R-PLACE3000194  
 R-PLACE3000197//ESTs//1.4e-38:197:98//Hs.146341:AI269930  
 R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.131370:AA927516  
 40 R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476  
 R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084  
 R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964  
 R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717  
 45 R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014  
 R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878  
 R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811  
 R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emericella nidulans]//7.5e-110:549:95//Hs.13692:AA632002  
 50 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307  
 R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:82//Hs.97203:U83171  
 R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782  
 R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP2K) mRNA, complete cds//4.0e-59:456:88//Hs.14666:U04811  
 R-PLACE3000320//Interleukin-10 (IL-10) PRECURSOR [Homo sapiens]//1.9e-42:288:85//Hs.2180:M57627  
 R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

114531:N74103

R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:AB018315

R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837

5 R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688

R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377

R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380

R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683

R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888

10 R-PLACE3000363

R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881

R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430

R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534

15 R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570

R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528

R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230

R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052160

R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108

20 R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87//Hs.73614:U83460

R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077

R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219

R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519

25 R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.153487:U43899

R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980

R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227

30 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:AB018352

R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240

R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031

R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292

35 R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444

R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547

R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739

R-PLACE4000100

40 R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:AB007931

R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-11:184:71//Hs.154278:N45985

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.118164:AB007969

45 R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582

R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:AB011147

R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186

50 R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734

R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949

R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080

R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219

R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216

R-PLACE4000261//EST//0.066:384:58//Hs.136284:AA400411

R-PLACE4000268//ESTs//0.000146:47//Hs.5000:H44587

R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782  
 R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131  
 R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454  
 R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460  
 5 R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414  
 R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478  
 R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656  
 R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425  
 R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-44:379:78//Hs.152369:AA504818  
 10 R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:AA778649  
 R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502  
 R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780  
 15 R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:AA643063  
 R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:72//Hs.1361:M55053  
 R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932  
 20 R-PLACE4000494//EST//1.4e-109:525:98//Hs.22539:AI334210  
 R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290  
 R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527  
 R-PLACE4000558//human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185  
 25 R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532  
 R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524  
 R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249  
 R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889  
 R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651  
 30 R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438  
 R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435  
 R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353  
 R-THYRO1000107//Interieuldn 10//2.8e-43:292:84//Hs.2180:M57627  
 R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359  
 35 R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108  
 R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764  
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:AF087142  
 40 R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217  
 R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426  
 R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258  
 R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946  
 45 R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189  
 R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219  
 R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219  
 R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:AJ005698  
 50 R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:AB014552  
 R-THYRO1000206//ESTs//3.1e-90:507:90//Hs.32456:W29063  
 R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-39:351:98//Hs.11000:AA68501  
 55 R-THYRO1000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

- R-THYRO1000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075  
 R-THYRO1000270//ESTs//1.9e-99:531:94//Hs.17767:N62925  
 R-THYRO1000279//EST//2.7e-54:266:99//Hs.149527:AI280674  
 5 R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566:91//Hs.25846:AB016068  
 R-THYRO1000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547  
 R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.80731:M63175  
 R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:AB018333  
 10 R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:U29091  
 R-THYRO1000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064  
 R-nnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250  
 R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:294:84//Hs.151614:AF032456  
 15 R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081  
 R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429  
 R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601  
 R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638  
 R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans]//8.5e-40:239:90//Hs.84009:AI309761  
 20 R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426  
 R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:AB018280  
 R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333  
 25 R-THYRO1000501//ESTs//L5e-46:287:89//Hs.125300:R62360  
 R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005  
 R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286:96//Hs.105861:AI206965  
 R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511  
 R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193  
 30 R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485  
 R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:AF075587  
 R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247  
 R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223  
 35 R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//Hs.21907:N24415  
 R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742  
 R-THYRO1000637  
 R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H. sapiens]//4.9e-46:245:95//Hs.97398:AA398634  
 40 R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840  
 R-nnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384  
 R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866  
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI061063  
 45 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109  
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713  
 R-THYRO1000712  
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287  
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713  
 50 R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624  
 R-THYRO1000777  
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932  
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897  
 55 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443111  
 R-THYRO1000805//EST//1.4e-107:44:77//Hs.23424:AA813594  
 R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067



R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172  
 R-THYRO1001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082  
 R-THYRO1001480//Small inducible cytokineA5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219  
 5 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135  
 R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110  
 R-THYRO1001537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094  
 10 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936  
 R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594  
 R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413  
 R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958  
 15 R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741  
 R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247  
 R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:288:67//Hs.85112:X57025  
 R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886  
 R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA: dihydroxyacetonephosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190  
 20 R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874  
 R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282  
 R-THYRO100166//ESTs//1.4e-56:323:91//Hs.24984:AA534446  
 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562:95//Hs.118633:AJ225089  
 25 R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957  
 R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726  
 R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691  
 30 R-THYRO1001721  
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184  
 R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172  
 R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323  
 R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474  
 35 R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224  
 R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788  
 R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956  
 R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123  
 40 R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314  
 R-VESEN1000122  
 R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289  
 R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI359321  
 45 R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178  
 R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs.153026:AB014540  
 R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629  
 R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792  
 50 R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159:AA113849  
 R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991  
 R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103  
 R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI421812  
 55 R-Y79AA1000231//ESTs//1.1e-108:526:97//Hs.82856:AI24681  
 R-Y79AA1000232//ESTs//1.1e-108:526:97//Hs.82856:AI24681  
 R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.44e-320:84//Hs.84123:AB002363  
 R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826

R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635  
 R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210  
 R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808  
 5 R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//  
 4.4e-66:339:97//Hs.8215:AA521150  
 R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-  
 44:279:88//Hs.139007:H74314  
 R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018  
 R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613  
 10 R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758  
 R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292  
 R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-  
 60:362:88//Hs.6381:AI188509  
 R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320  
 15 R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881  
 R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.  
 41723:U37426  
 R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848  
 R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:  
 20 AI125280  
 R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455  
 R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:  
 AF060503  
 R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC  
 25 REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818  
 R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586:  
 95//Hs.83023:AF093670  
 R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III  
 [C.elegans]//9.8e-111:563:95//Hs.19845:AI005330  
 30 R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405  
 R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463  
 R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433  
 R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359  
 R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512  
 35 R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642  
 R-nnnnnnnnnnnnn//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405  
 R-Y79AA1000805  
 R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227  
 R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650  
 40 R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.  
 55836:U85647  
 R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079  
 R-Y79AA1000968  
 R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181  
 45 R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049  
 R-Y79AA1000985  
 R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851  
 R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067  
 R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407  
 50 R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325  
 R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:  
 AB011135  
 R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047  
 R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260  
 55 R-Y79AA1001105//ESTs//6.5e-113:323:98//Hs.30891:H28113  
 R-Y79AA1001177//EST//1.2e-05:02:76//Hs.65277:T15864



- R-nnnnnnnnnnnn/ESTs//1.7e-55:478:76//Hs.154554:AA552715  
 R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.50441:AA747428  
 R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349  
 5 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//6.5e-86:518:90//Hs.25682:AA857843  
 R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274  
 R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977  
 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:  
 10 AB014592  
 R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102:507:96//Hs.25895:AI341537  
 R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555  
 R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288  
 15 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:AB014534  
 R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985  
 R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371  
 R-Y79AA1002361  
 20 R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908  
 R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000  
 R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753  
 R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026  
 R-nnnnnnnnnnnn/ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]  
 25 //4.4e-62:390:88//Hs.143930:AI207821  
 R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870  
 R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788  
 R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

## 30 Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

- C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%/Q61712  
 C-HEMBA1000030  
 40 C-HEMBA1000046  
 C-HEMBA1000050  
 C-HEMBA1000076  
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%/P08553  
 45 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3.-GAMMA (HNF-3G).//5E-16//166aa//36%/P35584  
 C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%/P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%/P48555  
 C-HEMBA1000193  
 C-HEMBA1000227  
 50 C-HEMBA1000288  
 C-HEMBA1000302  
 C-HEMBA1000304  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91 %//035594  
 C-HEMBA1000387  
 C-HEMBA1000392

C-HEMBA1000460  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN)//3.3E-45//481aa//29%//Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2//2E-22//188aa//31%//P22279  
 C-HEMBA1000501  
 5 C-HEMBA1000508  
 C-HEMBA1000520  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-  
 MENTS)//2.6E-12//73aa//41%//P02826  
 C-HEMBA1000534  
 10 C-HEMBA1000555  
 C-HEMBA1000568  
 C-HEMBA1000588  
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT)//1.8E-55//179aa//61%//O43295  
 C-HEMBA1000636  
 15 C-HEMBA1000682  
 C-HEMBA1000686  
 C-HEMBA1000719  
 C-HEMBA1000727  
 C-HEMBA1000752  
 20 C-HEMBA1000817  
 C-HEMBA1000851  
 C-HEMBA1000867  
 C-HEMBA1000869  
 C-HEMBA1000872  
 25 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//  
 1.6E-30//127aa//40%//P43366  
 C-HEMBA1000918  
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHRO-  
 MOSOME X//1E-10//288aa//23%//Q19124  
 30 C-HEMBA1000946  
 C-HEMBA1000968  
 C-HEMBA1000971  
 C-HEMBA1000975  
 C-HEMBA1001009  
 35 C-HEMBA1001022  
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT)//  
 1.4E-12//131aa//38%//Q01485  
 C-HEMBA1001052  
 C-HEMBA1001080  
 40 C-HEMBA1001085  
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN)//3.5E-50//  
 176aa//57%//P48059  
 C-HEMBA1001109  
 C-HEMBA1001122  
 45 C-HEMBA1001133  
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)  
 (FRAGMENT)//1.5E-116//197aa//58%//Q06730  
 C-HEMBA1001140  
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5//6.8E-79//179aa//80%//P51646  
 50 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds//9.5E-257//1307bp//94%//  
 AB020678  
 C-HEMBA1001235  
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase//0//1672bp//99%//AJ130733  
 C-HEMBA1001281  
 55 C-HEMBA1001282//Homo sapiens mRNA for KIAA0871 protein, complete cds//9.5E-257//1307bp//94%//  
 AB020678  
 C-HEMBA1001283//Homo sapiens mRNA for KIAA0871 protein, complete cds//9.5E-257//1307bp//94%//  
 AB020678  
 C-HEMBA1001310

- C-HEMBA1001326  
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358  
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081
- 5 C-HEMBA1001388  
 C-HEMBA1001398  
 C-HEMBA1001405  
 C-HEMBA1001407  
 C-HEMBA1001413
- 10 C-HEMBA1001415  
 C-HEMBA1001446  
 C-HEMBA1001450  
 C-HEMBA1001455  
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850
- 15 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166  
 C-HEMBA1001533  
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657  
 C-HEMBA1001581
- 20 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141  
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//Q63679  
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%//P33450
- 25 C-HEMBA1001702  
 C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386  
 C-HEMBA1001731  
 C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%//P53009
- 30 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675  
 C-HEMBA1001815  
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676  
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230  
 C-HEMBA1001864
- 35 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659  
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.3E-36//395aa//26%//Q63342  
 C-HEMBA1001987  
 C-HEMBA1002018
- 40 C-HEMBA1002049  
 C-HEMBA1002084  
 C-HEMBA1002125  
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//P79293
- 45 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//P43694  
 C-HEMBA1002191  
 C-HEMBA1002199  
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//P18161
- 50 C-HEMBA1002237  
 C-HEMBA1002265  
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537  
 C-HEMBA1002349  
 C-HEMBA1002363  
 C-HEMBA1002414  
 C-HEMBA1002430

- C-HEMBA1002439  
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%//Q00994  
 C-HEMBA1002460  
 C-HEMBA1002462  
 5 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175  
 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%//P17437  
 C-HEMBA1002477  
 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%//P48732  
 10 C-HEMBA1002515  
 C-HEMBA1002542  
 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%//AF075587  
 C-HEMBA1002583  
 15 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%//AB011169  
 C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%//AB018351  
 C-HEMBA1002688  
 C-HEMBA1002696  
 C-HEMBA1002750  
 20 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%//AJ000414  
 C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%//AB020636  
 C-HEMBA1002777  
 C-HEMBA1002794  
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185  
 25 C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1002850  
 C-HEMBA1002863  
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//1.5E-44//188aa//52%//Q09297  
 30 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%//AB011148  
 C-HEMBA1002937  
 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%//P16157  
 35 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%//AB020710  
 C-HEMBA1002954  
 C-HEMBA1002971  
 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%//P14646  
 40 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa//24%//Q02224  
 C-HEMBA1003033  
 C-HEMBA1003035  
 C-HEMBA1003041  
 C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//O75439  
 45 C-HEMBA1003067  
 C-HEMBA1003096  
 C-HEMBA1003117  
 C-HEMBA1003129  
 50 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%//P41940  
 C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%//AL079278  
 C-HEMBA1003150  
 C-HEMBA1003151//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%//AB011169  
 C-HEMBA1003152//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%//AB018351  
 C-HEMBA1003153//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%//AB011148  
 C-HEMBA1003154//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%//AB020636  
 C-HEMBA1003155//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185  
 C-HEMBA1003156//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003157//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003158//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003159//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003160//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003161//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003162//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003163//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003164//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003165//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003166//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003167//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003168//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003169//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003170//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003171//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003172//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003173//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003174//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003175//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003176//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003177//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003178//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003179//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003180//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003181//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003182//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003183//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003184//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003185//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003186//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003187//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003188//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003189//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003190//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003191//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003192//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003193//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003194//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003195//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003196//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003197//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003198//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819  
 C-HEMBA1003199//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819

- C-HEMBA1003222  
 C-HEMBA1003235//TROPOMYOSIN //0.0000023//109aa//33%//Q02088  
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-)//7.2E-41//245aa//42%//Q06548  
 C-HEMBA1003257  
 5 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR//6E-11//239aa//32%//P32506  
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds//5.4E-229//1043bp//99%//AB024436  
 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//0//791bp//99%//AB011109  
 C-HEMBA1003322  
 10 C-HEMBA1003327  
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//0.00000002//248aa//23%//Q02224  
 C-HEMBA1003370  
 C-HEMBA1003380  
 C-HEMBA1003395  
 15 C-HEMBA1003402  
 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds//0//1732bp//98%//AB020712  
 C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021)//1.6E-312//1414bp//99%//AL050287  
 C-HEMBA1003418//TRICHOHYALIN//8.7E-19//281aa//31%//P37709  
 20 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds//0//511bp//94%//AB013139  
 C-HEMBA1003447  
 C-HEMBA1003461  
 C-HEMBA1003463  
 C-HEMBA1003528  
 25 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2)//8.8E-189//360aa//96%//P50480  
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP)//2.1E-68//251aa//52%//P53384  
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-MA-I)//1.2E-31//71aa//100%//P16874  
 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//7.9E-49//279aa//32%//P19474  
 30 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1//6.9E-206//445aa//74%//Q13330  
 C-HEMBA1003581//TALIN//4.4E-45//52aa//98%//P26039  
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP)//4.4E-10//118aa//35%//P19682  
 35 C-HEMBA1003615  
 C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds//8.2E-178//501bp//97%//AB015344  
 C-HEMBA1003621  
 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2)//1.2E-75//151aa//99%//Q13207  
 C-HEMBA1003690//HISTONE DEACETYLASE HDA1//2.1E-59//249aa//47%//P53973  
 40 C-HEMBA1003711  
 C-HEMBA1003807  
 C-HEMBA1003864  
 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)//3.8E-16//89aa//46%//P16372  
 45 C-HEMBA1003959  
 C-HEMBA1003989  
 C-HEMBA1004074  
 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds//8.5E-221//1188bp//78%//AF091234  
 50 C-HEMBA1004146  
 C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds//0//1893bp//98%//AB023145  
 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds//0//1892bp//99%//U50748  
 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds//5.7E-217//1217bp//88%//AF095927  
 C-HEMBA1004234  
 C-HEMBA1004235  
 C-HEMBA1004236  
 C-HEMBA1004237  
 C-HEMBA1004238  
 C-HEMBA1004239

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C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955  
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//  
 AF089841  
 C-HEMBA1004596  
 5 C-HEMBA1004693  
 C-HEMBA1004736  
 C-HEMBA1004753  
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%//U49082  
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%//  
 10 L39060  
 C-HEMBA1004763  
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%//P08547  
 C-HEMBA1004771  
 C-HEMBA1004776  
 15 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P50851  
 C-HEMBA1004806  
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%//  
 Q00004  
 C-HEMBA1004850  
 20 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//  
 100%//AL080114  
 C-HEMBA1004923  
 C-HEMBA1004929  
 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401  
 25 C-HEMBA1004933  
 C-HEMBA1004954  
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
 0.00000096//286aa//23%//P12036  
 C-HEMBA1005475  
 30 C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270  
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//  
 151aa//37%//P16372  
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-  
 225//1189bp//88%//AF076183  
 35 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043  
 C-HEMBA1006377  
 C-HEMBA1006467  
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552  
 C-HEMBA1006530  
 40 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
 0.000000043//111aa//40%//Q01485  
 C-HEMBA1006795  
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258  
 C-HEMBA1006936  
 45 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//  
 AP078849  
 C-HEMBA1007342  
 C-HEMBA1000008  
 C-HEMBA1000018  
 50 C-HEMBA1000024  
 C-HEMBA1000025  
 C-HEMBA1000036  
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//  
 1582bp//80%//AF084928  
 55 C-HEMBA1000083  
 C-HEMBA1000084  
 C-HEMBA1000085  
 C-HEMBA1000086  
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- C-HEMBB1000136  
 C-HEMBB1000215  
 C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5//  
 2.7E-12//112aa//47%//Q09530  
 5 C-HEMBB1000244  
 C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-  
 MOSOME V.//6.1E-09//242aa//26%//Q23256  
 C-HEMBB1000338  
 C-HEMBB1000339  
 10 C-HEMBB1000391  
 C-HEMBB1000438  
 C-HEMBB1000449  
 C-HEMBB1000589  
 C-HEMBB1000591  
 15 C-HEMBB1000623  
 C-HEMBB1000630  
 C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//  
 232aa//28%//P78970  
 C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671  
 20 C-HEMBB1000671  
 C-HEMBB1000673  
 C-HEMBB1000705  
 C-HEMBB1000706  
 C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//  
 25 U53475  
 C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847  
 C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//  
 1.2E-126//613bp//97%//AF111105  
 C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-  
 30 54//232aa//43%//P39956  
 C-HEMBB1000807  
 C-HEMBB1000810  
 C-HEMBB1000848  
 C-HEMBB1000852  
 35 C-HEMBB1000870  
 C-HEMBB1000887  
 C-HEMBB1000908  
 C-HEMBB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102  
 C-HEMBB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp//  
 40 99%//AF116910  
 C-HEMBB1000973//Mus musculus schlafen3 (Sln3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974  
 C-HEMBB1000975  
 C-HEMBB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-  
 18//178aa//30%//P28575  
 45 C-HEMBB1000991  
 C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//  
 P51523  
 C-HEMBB1001014  
 C-HEMBB1001024  
 50 C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED  
 NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087  
 C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//  
 80%//AF010144  
 C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF001800  
 C-HEMBB1001096  
 C-HEMBB1001101  
 C-HEMBB1001120

- C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435  
 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267  
 C-HEMBB1001153  
 5 C-HEMBB1001169  
 C-HEMBB1001175//ANKYRIN//6.9E-11//169aa//31%//Q02357  
 C-HEMBB1001182  
 C-HEMBB1001199  
 C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187  
 10 C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897  
 C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966  
 C-HEMBB1001289  
 C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081  
 15 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%//U92703  
 C-HEMBB1001331  
 C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98175  
 C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%//AF097441  
 20 C-HEMBB1001369  
 C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-HEMBB1001387  
 C-MAMMA1002317  
 25 C-MAMMA1002319  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926  
 C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190  
 C-NT2RM1000242  
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028  
 30 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P39942  
 C-NT2RM1000669  
 C-NT2RM1000781  
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%//AF092138  
 35 C-NT2RM1001008  
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//980bp//95%//AF085360  
 C-NT2RM1001074  
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14)//0.0000056//239aa//27%//  
 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete sequence.//0//1740bp//99%//AL031291  
 40 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167  
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703  
 45 C-NT2RM2000032  
 C-NT2RM2000042  
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%//P50102  
 50 C-NT2RM2000093  
 C-NT2RM2000101  
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223  
 C-NT2RM2000192  
 C-NT2RM2000255  
 C-NT2RM2000256//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223  
 C-NT2RM2000259

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//3.6E-19//181-aa//34%//  
P14918

C-NT2RM2000287

C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//  
AB020666

C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132

C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274

C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//  
U48251

C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLE-  
OTIDE//1.7E-68//419aa//36%//P50849

C-NT2RM2000374

C-NT2RM2000395

C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-  
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-  
NENT)//1.6E-54//344aa//33%//P32802

C-NT2RM2000407

C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//  
Q08469

C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//  
157aa//28%//P36113

C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-) //0.0000089//377aa//24%//  
P22211

C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823

C-NT2RM2000502

C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243

C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//  
32%//P17437

C-NT2RM2000540

C-NT2RM2000567

C-NT2RM2000569

C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//  
1.7E-187//741aa//46%//P73505

C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D86987

C-NT2RM2000588//HISTONE DEACETYLASE HDA1 //2.8E-60//384aa//40%//P53973

C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//  
0//2712bp//99%//AF156487

C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//  
AF179221

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
SRP75).//4.4E-32//319aa//35%//Q08170

C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272

C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558

C-NT2RM2000639

C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576

C-NT2RM2000669

C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391

C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//  
36%//Q15404

C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342

C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//  
P41877

C-NT2RM2000795

C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-276//545aa//  
39%//P23511

C-NT2RM2000855

C-NT2RM2000856//Homo sapiens mRNA for KIAA0658 protein, complete cds.//1.7E-200//927bp//99%//  
AB015046

- C-NT2RM2000952  
 C-NT2RM2000984  
 C-NT2RM2001004  
 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809  
 5 C-NT2RM2001065  
 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//  
 26%//P46577  
 C-NT2RM2001131  
 C-NT2RM2001141  
 10 C-NT2RM2001152  
 C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//  
 1335bp//99%//AL080109  
 C-NT2RM2001194  
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143  
 15 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//  
 P48724  
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//  
 32%//P97924  
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
 20 DOHYDROLASE).//1.3E-180//328aa//99%//P13264  
 C-NT2RM2001243  
 C-NT2RM2001247  
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//  
 P53995  
 25 C-NT2RM2001291  
 C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%//  
 AL080063  
 C-NT2RM2001312  
 C-NT2RM2001319  
 30 C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584  
 C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%//000808  
 C-NT2RM2001370  
 C-NT2RM2001393  
 C-NT2RM2001420  
 35 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//  
 100%//AL050146  
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//  
 437aa//57%//P52569  
 C-NT2RM2001504  
 40 C-NT2RM2001524  
 C-NT2RM2001544  
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//  
 90aa//42%//P38660  
 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-  
 45 61//312aa//44%//P19474  
 C-NT2RM2001582  
 C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610  
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692  
 C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931  
 50 C-NT2RM2001930  
 C-NT2RM2001935  
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320  
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//  
 212aa//23%//P38250  
 C-NT2RM2001956  
 C-NT2RM2001957//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

28%/Q12730

C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%/Q09782

C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.000000029//83aa//44%/P40796

C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%/P46837

C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%/AB016789

C-NT2RM2002049

C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%/Q07878

C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%/Q61990

C-NT2RM2002091

C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840

C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%/AF030435

C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%/P49695

C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805

C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%/AL117402

C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%/P25167

C-NT2RM4000061

C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%/P52742

C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%/X68101

C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%/P25386

C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%/P16381

C-NT2RM4000197

C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%/AB018255

C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%/L20303

C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%/M99438

C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%/AJ132637

C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%/AF083246

C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%/Q24371

C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%/AB025412

C-NT2RM4000395

C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769

C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8E-20//393aa//24%/Q10297

C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%/AF097025

C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%/P04280

C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%/P39955

C-NT2RM4000511

C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%/P16884

C-NT2RM4000520

C-NT2RM4000581

C-NT2RM4000585//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%/AB014587

C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%/AB014587

- C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000040  
 C-NT2RP1000063  
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834  
 5 C-NT2RP1000101  
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471  
 C-NT2RP1000112  
 C-NT2RP1000124  
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859  
 10 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165  
 C-NT2RP1000170  
 C-NT2RP1000191  
 C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357  
 C-NT2RP1000243  
 15 C-NT2RP1000259  
 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730  
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551  
 20 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447  
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343  
 C-NT2RP1000357  
 C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%//AL080187  
 25 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159  
 C-NT2RP1000416  
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423  
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257  
 30 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580  
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653  
 C-NT2RP1000481  
 35 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686  
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020  
 C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367  
 40 C-NT2RP1000581  
 C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233  
 C-NT2RP1000688  
 C-NT2RP1000695  
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379  
 45 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434  
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566  
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960  
 50 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223  
 C-NT2RP1000846  
 C-NT2RP1000851  
 C-NT2RP1000852//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000853//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000854//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000855//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000856//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000857//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000858//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000859//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000860//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000861//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000862//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000863//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000864//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000865//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000866//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000867//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000868//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000869//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000870//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000871//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000872//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000873//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000874//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000875//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000876//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000877//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000878//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000879//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000880//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000881//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000882//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000883//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000884//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000885//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000886//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000887//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000888//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000889//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000890//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000891//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000892//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000893//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000894//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000895//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000896//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000897//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000898//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000899//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000900//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000901//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000902//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000903//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000904//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000905//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000906//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000907//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000908//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000909//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000910//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000911//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000912//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000913//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000914//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000915//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000916//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000917//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000918//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000919//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000920//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000921//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000922//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000923//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000924//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000925//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000926//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000927//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000928//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000929//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000930//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000931//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000932//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000933//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000934//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000935//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000936//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000937//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000938//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000939//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000940//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000941//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000942//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000943//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000944//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000945//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000946//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657  
 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbCH5B (UBCH5B) mRNA, complete cds.//4.6E-

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN)//1.4E-23//370aa//28%//Q04652

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//  
M17885

C-NT2RP1000980

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//1529bp//61%//L01790

C-NT2RP1001395

C-NT2RP1001424

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%//AJ005257

C-NT2RP1001475

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891

C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN) //1.6E-30//232aa//30%//035566

C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)//5.8E-121//271aa//89%//P47758

C-NT2RP1001616

C-NT2RP1001665//CALMODULIN./0.00000051//83aa//30%/P02594

C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%//Q34136

C-NT2RP2000007

C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//P51523

C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1)//1.8E-22//184aa//34%//Q01730

C-NT2R2P2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.  
0//1390bp//98%//AF061749

C-NT2RP2000054

C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-SILON)//9.4E-16//45aa//100%//P49446

C-NT2RP2000067

C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//383aa//32%/P33450

C-NT2RP2000079

C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338

C-NT2RP2000091

C-NT2RP2000097

C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds./0//2244bp//99%//AB018356

C-NT2RP2000120

C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L//2.5E-117//541aa//42%//P41877

C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206

C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN 47) (GOLGI APPARATUS) (PACIFIC NORTHWEST NATIONAL LABORATORY)

SEMBL: [EMBL](#) [JMP167](#) MEDIUM CHAIN 164 4E-226/423aa 100% D35588

J2RP200553/GAR2 PROTEIN/9 8E-23/311aa/28%/P41891

NT2RP2000157//MLO2 PROTEIN//2.6E-11//62aa//40%//Q09329

C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%//  
 AB023225  
 C-NT2RP2000173  
 C-NT2RP2000175  
 5 C-NT2RP2000195  
 C-NT2RP2000205  
 C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699  
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568  
 C-NT2RP2000232  
 10 C-NT2RP2000233  
 C-NT2RP2000239  
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE  
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558  
 C-NT2RP2000270  
 15 C-NT2RP2000274  
 C-NT2RP2000283  
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1.//1.6E-27//576aa//  
 25%//Q10297  
 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676  
 20 C-NT2RP2000298  
 C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//  
 1193bp//99%//U82381  
 C-NT2RP2000328  
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//  
 25 226aa//92%//P08760  
 C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//  
 674aa//46%//P17564  
 C-NT2RP2000369  
 C-NT2RP2000412  
 30 C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//  
 100%//P52597  
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//  
 99%//AF102265  
 C-NT2RP2000438  
 35 C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844  
 C-NT2RP2000503  
 C-NT2RP2000510  
 C-NT2RP2000516  
 C-NT2RP2000603  
 40 C-NT2RP2000617  
 C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514  
 C-NT2RP2000656  
 C-NT2RP2000658  
 C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577  
 45 C-NT2RP2000704  
 C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE).//2.7E-100//  
 488aa//44%//Q32038  
 C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623  
 C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680  
 50 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//  
 29%//Q99104  
 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//  
 P13466  
 C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174  
 55 C-NT2RP2000819  
 C-NT2RP2000840  
 C-NT2RP2000863

C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2//0//694aa//99%//060841  
 C-NT2RP2000892  
 C-NT2RP2000931//MATRIN 3//2.4E-289//467aa//95%//P43244  
 C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043)//0//2487bp//99%//  
 5 AL050390  
 C-NT2RP2000938  
 C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//0//3458bp//99%//AB018298  
 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds//0//1989bp//96%//AB024704  
 C-NT2RP2000985  
 10 C-NT2RP2001036  
 C-NT2RP2001044  
 C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//0//2749bp//99%//  
 AB007957  
 C-NT2RP2001065  
 15 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE)//  
 5.8E-46//222aa//45%//Q20939  
 C-NT2RP2001081//SYNAPTOTAGMIN IV//4.2E-118//430aa//54%//P50232  
 C-NT2RP2001094  
 C-NT2RP2001119  
 20 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein//0//2514bp//99%//AJ132440  
 C-NT2RP2001218  
 C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC)//  
 2.2E-10//366aa//28%//P14105  
 C-NT2RP2001381  
 25 C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174)//0//1495bp//  
 100%//AL080146  
 C-NT2RP2001427  
 C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//0//1748bp//99%//AB018340  
 C-NT2RP2001675  
 30 C-NT2RP2001721  
 C-NT2RP2001907  
 C-NT2RP2001969  
 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds//4.7E-177//  
 1538bp//74%//AF062378  
 35 C-NT2RP2002046  
 C-NT2RP2002154  
 C-NT2RP2002208  
 C-NT2RP2002270//AF-9 PROTEIN//0.00000012//74aa//36%//P42568  
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein//0//2333bp//99%//Y16521  
 40 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds//8.4E-254//1158bp//99%//AB015594  
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//4.3E-240//  
 1105bp//99%//AF038958  
 C-NT2RP2002426  
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//0//2180bp//99%//  
 45 AB005289  
 C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X//6.2E-19//288aa//26%//  
 Q11073  
 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257)//7.5E-35//181aa//  
 42%//P12815  
 50 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-)//1.7E-51//326aa//38%//  
 P55345  
 C-NT2RP2002621  
 C-NT2RP2002672  
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II//1.3E-14//316aa//  
 100%//Q14345  
 C-NT2RP2002852//HYPOTHETICAL 34 KD PROTEIN INDUCED 34 KD PROTEIN//8.8E-10//  
 203aa//27%//P29764

C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//  
 100%//AF038392  
 C-NT2RP2002954  
 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 5 LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//4.6E-80//147aa//100%//P51669  
 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129  
 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//  
 AB026190  
 C-NT2RP2003108  
 10 C-NT2RP2003117  
 C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds.//2.3E-82//642bp//68%//  
 AF079765  
 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN)//2.4E-38//539aa//25%//004652  
 C-NT2RP2003177  
 15 C-NT2RP2003194  
 C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811  
 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//  
 AB006572  
 C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//  
 20 P26337  
 C-NT2RP2003367  
 C-NT2RP2003433//PROTEIN TRANSPORT PROTFIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378  
 C-NT2RP2003446  
 C-NT2RP2003533  
 25 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-)//1.7E-17//  
 148aa//34%//P74261  
 C-NT2RP2003596  
 C-NT2RP2003629  
 C-NT2RP2003687  
 30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//5.4E-29//85aa//72%//  
 Q05481  
 C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//1.7E-75//147aa//93%//P51669  
 C-NT2RP2003793  
 35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMI-  
 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)//1.5E-23//200aa//30%//O09175  
 C-NT2RP2003986  
 C-NT2RP2004042  
 C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered  
 40 pieces.//8.2E-202//926bp//100%//AL096820  
 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//  
 126aa//39%//P38120  
 C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044  
 C-NT2RP2004463  
 45 C-NT2RP2004602  
 C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139  
 C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291  
 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa//  
 33%//Q92355  
 50 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA  
 LIGASE) (LEURS)//9.5E-73//153aa//59%//Q10490  
 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC  
 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA)//3.7E-135//414aa//62%//P53588  
 C-NT2RP2004802  
 C-NT2RP2004814  
 C-NT2RP2004931  
 C-NT2RP2004959//Homo sapiens mRNA PRECURSOR.//0.000000095//297aa//20%//P13692  
 C-NT2RP2004999

C-NT2RP2005000

C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%//AB014515

C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779

C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%//P32447

5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743

C-NT2RP2005140

C-NT2RP2005147

C-NT2RP2005159

10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025

C-NT2RP2005270

C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053

C-NT2RP2005293

C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576

15 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247

C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823

C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%//Q08170

20 C-NT2RP2005441

C-NT2RP2005453

C-NT2RP2005464

C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127

C-NT2RP2005472

25 C-NT2RP2005495

C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803

C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563

30 C-NT2RP2005525//Mus musculus kanadapin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526

C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39366

35 C-NT2RP2005555

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085

40 C-NT2RP2005622

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623

C-NT2RP2005637

C-NT2RP2005640

45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//P56101

C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973

C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%//AF089814

C-NT2RP2005683

50 C-NT2RP2005690

C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342

C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.000000003//169aa//28%//P38074

C-NT2RP2005748

C-NT2RP2005750

C-NT2RP2005751

C-NT2RP2005752//Homo sapiens G-protein coupled receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)//1.7E-61//374aa//38%//P47943  
 C-NT2RP2005767//G.gallus PB1 gene//5E-163//1158bp//81%//X90849  
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds//  
 2.7E-180//656bp//99%//AF151351  
 5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-  
 CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-  
 BINDING PROTEIN) (SABP)//2.1E-213//249aa//85%//Q02038  
 C-NT2RP2005781  
 C-NT2RP2005804  
 10 C-NT2RP2005835//SHP1 PROTEIN//1.8E-28//208aa//32%//P34223  
 C-NT2RP2005853  
 C-NT2RP2005868  
 C-NT2RP2005886  
 C-NT2RP2005890  
 15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds//0//1977bp//99%//AB023188  
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57)//5E-11//155aa//34%//P48837  
 C-NT2RP2006038  
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75)//1.5E-13//185aa//38%//Q08170  
 20 C-NT2RP2006052  
 C-NT2RP2006069  
 C-NT2RP2006071  
 C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102)//0//1759bp//  
 99%//AL049970  
 25 C-NT2RP2006106  
 C-NT2RP2006141  
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//3.3E-189//899bp//97%//AB014554  
 C-NT2RP2006196  
 C-NT2RP2006200  
 30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.1E-214//1026bp//97%//X96484  
 C-NT2RP2006237  
 C-NT2RP2006238  
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1]//2E-59//  
 388aa//32%//P46821  
 35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.8E-274//1236bp//99%//AF035262  
 C-NT2RP2006333  
 C-NT2RP2006365  
 C-NT2RP2006393  
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX)//  
 0.00000034//50aa//50%//Q61658  
 40 C-NT2RP2006456  
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//0//2181bp//99%//AJ006266  
 C-NT2RP2006467  
 C-NT2RP2006472  
 45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein//0//1276bp//84%//Y15710  
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 50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds//0//2547bp//99%//AB020708  
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 5 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//2E-111//  
 226aa//92%/P08760  
 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1  
 and Prp6//0//2072bp//98%/AB019219  
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18//2.1E-107//206aa//99%/P35293  
 10 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//  
 1.7E-139//679aa//41%/O43143  
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//0//2364bp//99%/AF071185  
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 15 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN)//1.9E-12//192aa//30%/P15151  
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 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR//7E-28//176aa//34%/Q94650  
 25 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN//2.5E-36//417aa//31%/Q61982  
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 35 C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds//0//3199bp//99%/AF064257  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds//  
 2.7E-185//585bp//88%/AF015264  
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 40 STAUFEN//0.00000006//78aa//48%/P25159  
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 C-NT2RP3001081  
 C-NT2RP3001084  
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds//1.7E-94//787bp//66%/AF087433  
 45 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN)//3E-44//260aa//40%/P55201  
 C-NT2RP3001109  
 C-NT2RP3001116  
 C-NT2RP3001119  
 C-NT2RP3001133  
 50 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//0//2802bp//99%/AB018305  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//0//2732bp//99%/AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION//1.7E-10//  
 196aa//27%/P53154  
 C-NT2RP3001214  
 C-NT2RP3001221//GAMMA-BUTYROBETAINE 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-  
 BUTYROBETAINE HYDROXYLASE)//1.9E-31//353aa//30%/P80193

C-NT2RP3001236

C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1]//1.2E-166//395aa//51%//P14873

C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%//AB020718

C-NT2RP3001307

C-NT2RP3001325

C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%//AB025905

C-NT2RP3001392

C-NT2RP3001396

C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF//1.3E-61//374aa//36%//P49711

C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009

C-NT2RP3001420

C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT)//1E-16//77aa//46%//O33529

C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%//O09053

C-NT2RP3001457

C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A//9.1E-13//87aa//43%//P11632

C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395

C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801

C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%//P20964

C-NT2RP3001621

C-NT2RP3001629

C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%//Q92609

C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa//31%//O22468

C-NT2RP3001676

C-NT2RP3001679

C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE//1.6E-11//348aa//27%//P24733

C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN)//7.4E-18//249aa//30%//Q04652

C-NT2RP3001896

C-NT2RP3001915

C-NT2RP3001929

C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%//P52742

C-NT2RP3004466

C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E-113//466aa//42%//P34110

C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%//AB014532

C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%//AB011126

C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID)//0.000000038//150aa//28%//Q01484

C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%//AF026445

C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%//AB007946

C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266

C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%//Q02084

C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097

C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN)//1.7E-72//254aa//45%//P54352

C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%//P35526

C-NT2RP4000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65.//4.9E-51//335aa//37%//Q64375

C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%//AB020657

C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538

C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100KD SUBUNIT

C-NT2RP4000124

C-NT2RP4000124

C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150

C-NT2RP4000151

C-NT2RP4000159

C-NT2RP4000185

5 C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%//AB014600

C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%//P15287

C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470

C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173

10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968

C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1.//3.5E-297//1024aa//55%//P87115

C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631

15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//32%//P26372

C-NT2RP4000355

C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%//AB018281

20 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195

C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%//O75570

C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243

C-NT2RP4000381

25 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738

C-NT2RP4000415

C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701

30 C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%//AL050078

C-NT2RP4000449

C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309

C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%//P50101

35 C-NT2RP4000480

C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%//Q09475

C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484

40 C-NT2RP4000500

C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818

C-NT2RP4000524

C-NT2RP4000541

C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319

45 C-NT2RP4000560

C-NT2RP4000588

C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%//AF067730

C-NT2RP4000638

50 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%//P09309

C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//30%//P39625

C-NT2RP4000704

C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-101//551aa//32%//P40319

C-NT2RP4000724

C-NT2RP4000724//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//1994bp//99%//AB023120

C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%//AB023146

C-NT2RP4000737

C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229  
C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000032//67aa//31%//P53915  
C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939  
C-NT2RP4000833  
C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265  
C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808  
C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175  
C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415  
C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682  
C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314  
C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//227aa//36%//Q06828  
C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.5E-76//346aa//43%//Q61068  
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521  
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900  
C-NT2RP4000955  
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//90aa//42%//P38660  
C-NT2RP4000975  
C-NT2RP4000979  
C-NT2RP4000984  
C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579  
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700  
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968  
C-NT2RP4001006  
C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181  
C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE).//1.5E-92//443aa//44%//Q09996  
C-NT2RP4001057  
C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375  
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//563aa//46%//P13586  
C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967  
C-NT2RP4001086  
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400  
C-NT2RP4001100  
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//P38378  
C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736  
C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283  
C-NT2RP4001138  
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP).//0.00000021//93aa//33%//P44514  
C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750  
C-NT2RP4001149  
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.4E-29//385aa//29%//P35331  
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001175//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001176//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001177//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001178//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001179//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001180//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001181//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001182//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001183//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001184//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001185//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001186//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001187//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001188//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001189//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001190//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001191//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001192//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001193//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001194//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001195//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001196//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001197//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001198//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001199//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331  
C-NT2RP4001200//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (OTST).//1.7E-22//227aa//36%//P35331

- C-NT2RP4001210  
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//6.2E-27//90aa//42%/P38660  
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)//1.8E-103//508aa//43%/Q04652
- 5 C-NT2RP4001235  
C-NT2RP4001256  
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%/AB020682  
C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%/U49082  
C-NT2RP4001276//TRICHOHYALIN//7.9E-09//126aa//32%/Q07283
- 10 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT)//5.9E-17//296aa//29%/P24391  
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%/AJ001119  
C-NT2RP4001339//Homo sapiens mRNA for AMMER1 protein.//9.2E-160//736bp//99%/AJ007014
- 15 C-NT2RP4001343  
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%/AB017494  
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%/U53445
- 20 C-NT2RP4001353  
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//1.6E-19//222aa//30%/Q08180  
C-NT2RP4001373  
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1)//9.2E-17//146aa//35%/P18160
- 25 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2E-53//436aa//30%/Q10085  
C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%/AB023140  
C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//7.7E-190//422aa//82%/Q14141
- 30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.2E-138//419aa//54%/Q99676  
C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%/AF129131  
C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE)//0//962aa//78%/Q02218
- 35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%/P39010  
C-NT2RP4001502  
C-NT2RP4001507  
C-NT2RP4001524  
C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-54//242aa//3.8%/P25656
- 40 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%/AF152961  
C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-)//4.7E-09//216aa//24%/P96902  
C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26%/Q02453
- 45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%/P35197  
C-NT2RP4001571  
C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%/AF100756  
C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%/AJ223830  
C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//1.7E-141//373aa//47%/P73505
- 50 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%/AB020676  
C-NT2RP4001614  
C-NT2RP4001634  
C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%/P40157  
C-NT2RP4001641//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%/AB020676  
C-NT2RP4001642//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%/AB020676  
C-NT2RP4001657  
C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF

100 KD SUBUNIT)//4E-10//243aa//25%/Q10568

C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//3E-10//128aa//32%/Q10282

C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT)//6.4E-170//1168aa//33%/Q09332

C-NT2RP4001739

C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//3.9E-236//665aa//58%/P51523

C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN)//4.1E-16//263aa//27%/P98174

C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds//0//3144bp//99%/AB023232

C-NT2RP4001803

C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)//1.2E-30//241aa//30%/O35566

C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4//1.1E-19//77aa//54%/P55083

C-NT2RP4001828

C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds//6.3E-99//555bp//73%/AF155595

C-NT2RP4001861//TRICHOHYALEN//1E-35//307aa//34%/P37709

C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043)//0//1306bp//98%/AL050390

C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1//0.000000014//345aa//25%/Q00808

C-NT2RP4001901

C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1//1.3E-38//258aa//32%/Q12024

C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF//9.8E-60//303aa//38%/P49711

C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA- ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO- ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)//1.5E-13//211aa//28%/Q43209

C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//1.2E-13//356aa//27%/P13816

C-NT2RP4001953

C-NT2RP4001966

C-NT2RP4001975

C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN)//6.9E-24//370aa//27%/Q04652

C-NT2RP4002052

C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1E-137//679aa//40%/O43143

C-NT2RP4002071

C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//3E-150//722aa//39%/Q05481

C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL)//0.0000067//250aa//31%/P52655

C-NT2RP4002298

C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-)//1.5E-63//159aa//53%/P38938

C-NT2RP4002791

C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434F172 (from clone DKFZp434F172)//0//2557bp//99%/AL080202

C-NT2RP4002905

C-NT2RP5003461//RLR1 PROTEIN//9.7E-22//177aa//27%/P53552

C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1//5.5E-15//280aa//27%/Q00808

C-NT2RP5003492

C-NT2RP5003500

C-NT2RP5003506

C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)//3.3E-23//219aa//40%/P37116

C-NT2RP5003534

C-OVARC1000006//HISTONE H2A//1E-55//117aa//99%/P02262

C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1)//0.0000042//102aa//32%/P37116

O14727

C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922

C-OVARC1000035

C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//  
5 0.00000032//60aa//45 %//P80022

C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874

C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//  
8.4E-14//259aa//30%//P51610

C-OVARC1000113

C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955

C-OVARC1000148

C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.//  
2.5E-95//461bp//98%//AJ242975

C-OVARC1000168

C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%//  
AF068332

C-OVARC1000212

C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
(MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU-  
20 CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa//  
30%//P14904

C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249

C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363

C-OVARC1000321

C-OVARC1000326

C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//  
200aa//27%//P40004

C-OVARC1000347

C-OVARC1000384

C-OVARC1000411

C-OVARC1000420

C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205

C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//  
35 99%//AL080126

C-OVARC1000461

C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075

C-OVARC1000466

C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-  
40 CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452

C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636

C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850

C-OVARC1000564

C-OVARC1000576

C-OVARC1000588

C-OVARC1000605

C-OVARC1000640

C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-  
plete cds.//0//1812bp//98%//D43772

C-OVARC1000661

C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886

C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343

C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533

C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//A1130978

C-OVARC1001044//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//A1130978

C-OVARC1001151

C-OVARC1001243

C-OVARC1001296

C-OVARC1001360  
 C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//6E-148//683bp//99%//AJ224819  
 C-OVARC1001425  
 5 C-PLACE1000005  
 C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%//P53538  
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.8E-29//134aa//43%//P52046  
 10 C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5e-312//1411bp//99%//AB020639  
 C-PLACE1000185  
 C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%//AB023194  
 C-PLACE1000347  
 C-PLACE1000374  
 15 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%//AB020660  
 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979  
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30//352aa//31%//P15151  
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//72%//P23246  
 20 C-PLACE1000420//7.8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//0.0000028//134aa//29%//P53368  
 C-PLACE1000435  
 C-PLACE1000444  
 C-PLACE1000562  
 25 C-PLACE1000564  
 C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.6E-270//437aa//86%//P32455  
 C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%//AB020657  
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%//AF044201  
 30 C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%//Q08891  
 C-PLACE1000716  
 C-PLACE1000748  
 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete-cds.//4.6E-250//1189bp//97%//AB028449  
 35 C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%//AB014548  
 C-PLACE1000798  
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.5E-49//181aa//54%//P32899  
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%//P39010  
 40 C-PLACE1000948  
 C-PLACE1000972  
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%//Q03070  
 C-PLACE1001000  
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485  
 45 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%//Q04652  
 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-UIEM).//3E-33//138aa//42%//Q61103  
 C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//132aa//46%//Q12929  
 50 C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0//2118bp//99%//AC005412  
 C-PLACE1001412  
 C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered pieces.//0//1440bp//99%//AF031660  
 C-PLACE1001517  
 C-PLACE1001610  
 C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)

(THIOESTERASE n).//4E-81//263aa//56%//P08635

C-PLACE1001729

C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.5E-75//439aa//41%//P16381

C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%//Q57290

C-PLACE1001810

C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953

C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524

C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%//AF131737

C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935

C-PLACE1001928

C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091

C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211

C-PLACE1002072

C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//0.00000053//188aa//29%//P49606

C-PLACE1002140

C-PLACE1002163

C-PLACE1002170

C-PLACE1002433

C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105

C-PLACE1002465

C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256

C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180

C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%//Q15391

C-PLACE1002794

C-PLACE1002815

C-PLACE1002839

C-PLACE1002851

C-PLACE1002941

C-PLACE1002996

C-PLACE1003045

C-PLACE1003092

C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268

C-PLACE1003108

C-PLACE1003145

C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743

C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750

C-PLACE1003200

C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//99%//AL080133

C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//P51522

C-PLACE1003334

C-PLACE1003342

C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715

C-PLACE1003369

C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200

C-PLACE1003611

C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN //3.2E-10//380aa//25%//P18824

C-PLACE1003764//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//99%//AL080133

C-PLACE1003775//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//99%//AL080133

C-PLACE1003777

C-PLACE1003723

- C-PLACE1003762  
 C-PLACE1003771  
 C-PLACE1003784  
 C-PLACE1003923  
 5 C-PLACE1003936  
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//  
 2.4E-124//326aa//73%/P80385  
 C-PLACE1004104  
 C-PLACE1004114  
 10 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA  
 CHAIN 4).//6.1E-181//340aa//96%/P29387  
 C-PLACE1004149  
 C-PLACE1004156  
 C-PLACE1004161  
 15 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%/AJ010071  
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%/Q62556  
 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//  
 0//1882bp//99%/AF069493  
 C-PLACE1004258  
 20 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%/O15393  
 C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp//99%/  
 AF084830  
 C-PLACE1004289  
 C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%/P33750  
 25 C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%/Y11588  
 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//  
 2512bp//99%/AF100153  
 C-PLACE1004376  
 C-PLACE1004388  
 30 C-PLACE1004405  
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%/Q63448  
 C-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene  
 encoding mitochondrial protein, complete cds.//0//985bp//99%/U49283  
 C-PLACE1004451  
 35 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%/P25823  
 C-PLACE1004473  
 C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete//1.3E-209//954bp//  
 99%/AF026445  
 C-PLACE1004516  
 40 C-PLACE1004548  
 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100  
 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%/Q10568  
 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%/Q13438  
 C-PLACE1004645  
 45 C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%/X  
 66277  
 C-PLACE1004664  
 C-PLACE1004672  
 C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//  
 50 96%/P12815  
 C-PLACE1004691  
 C-PLACE1004722  
 C-PLACE1004736  
 C-PLACE1004740  
 C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal V. complete cds.//7.1E-224//  
 790bp//98%/AB022918

- C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN)//1.9E-32//259aa//32%//P30337
- C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)//4.7E-65//695aa//29%//Q01631
- 5 C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//5.9E-19//196aa//36%//Q08170
- C-PLACE1004824
- C-PLACE1004868//MALE STERILITY PROTEIN 2//3.9E-39//261aa//27%//Q08891
- C-PLACE1004885
- 10 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C//9.3E-11//94aa//47%//O42643
- C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA)//4.9E-48//198aa//44%//P06151
- C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936
- 15 C-PLACE1004934
- C-PLACE1004937//SEL-10 PROTEIN//6.3E-125//357aa//58%//Q93794
- C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X//2E-14//205aa//26%//Q11073
- C-PLACE1004982
- 20 C-PLACE1005026
- C-PLACE1005027
- C-PLACE1005046
- C-PLACE1005077
- C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//1E-209//1031bp//96%//L40401
- 25 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN)//2.6E-56//565aa//30%//Q04652
- C-PLACE1005111
- C-PLACE1005181
- C-PLACE1005187//APAG PROTEIN//3.8E-13//122aa//36%//P05636
- C-PLACE1005206
- 30 C-PLACE1005232
- C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//1.3E-27//349aa//32%//Q01577
- C-PLACE1005261
- C-PLACE1005266
- C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.2E-297//1341bp//100%//AB011182
- 35 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP)//2.3E-13//269aa//28%//P53352
- C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//2E-111//226aa//92%//P08760
- C-PLACE1005308
- C-PLACE1005313
- 40 C-PLACE1005327
- C-PLACE1005335
- C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)//8.6E-09//194aa//27%//O33335
- 45 C-PLACE1005374
- C-PLACE1005480
- C-PLACE1005481
- C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6//0//1649bp//99%//AJ006276
- 50 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III//5.6E-52//173aa//57%//Q09251
- C-PLACE1005550
- C-PLACE1005554
- C-PLACE1005623
- C-PLACE1005625
- C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE)//2.1E-148//321aa//83%//P31350

- C-PLACE1005730  
C-PLACE1005755  
C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II)//2.5E-79//209aa//53%//P08635
- 5 C-PLACE1005803  
C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//1.1E-217//994bp//99%//AF027156  
C-PLACE1005851  
C-PLACE1005921//AIG1 PROTEIN//3E-31//284aa//31%//P54120
- 10 C-PLACE1005923  
C-PLACE1005925  
C-PLACE1005934  
C-PLACE1005936  
C-PLACE1005951
- 15 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//6.7E-30//198aa//37%//P43636  
C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-54//455aa//32%//P14904  
C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)//0.00000014//254aa//25%//P38129
- 20 C-PLACE1005990  
C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2//0//1564bp//99%//AJ236876  
C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//4.7E-161//744bp//99%//X99906  
C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//1.5E-148//681bp//99%//AF039023
- 25 C-PLACE1006139  
C-PLACE1006159  
C-PLACE1006167  
C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds//4.5E-293//953bp//99%//AB020706  
C-PLACE1006195
- 30 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06//2.7E-116//496aa//48%//Q09747  
C-PLACE1006225  
C-PLACE1006236  
C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN)//2E-16//244aa//31%//P28675
- 35 C-PLACE1006246  
C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142)//3.8E-278//1271-bp//99%//AL080066  
C-PLACE1006335  
C-PLACE1006357
- 40 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds//0//1168bp//99%//AF062085  
C-PLACE1006412  
C-PLACE1006414  
C-PLACE1006438//ZINC FINGER PROTEIN 165//2.5E-45//122aa//43%//P49910  
C-PLACE1006445
- 45 C-PLACE1006470  
C-PLACE1006482//TRANSCRIPTION FACTOR MAFF//7.7E-55//142aa//85%//Q90595  
C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)//1.1E-229//367aa//96%//Q00004  
C-PLACE1006492
- 50 C-PLACE1006531  
C-PLACE1006552  
C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces//0//2182bp//99%//AC007383  
C-PLACE1006615  
C-PLACE1006624  
C-PLACE1006671  
C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone HP10328//5.8E-24//734bp//62%//AB015630

C-PLACE1006704

C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE) //6.9E-13//177aa//33%//Q59263

C-PLACE1006782

5 C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //9.8E-213//232aa//80%//P08547

C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN) //2E-15//188aa//29%//P35123

C-PLACE1006883

10 C-PLACE1006901

C-PLACE1006917//HSH49 PROTEIN //5.5E-12//97aa//35%//Q99181

C-PLACE1006932

C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III //6.7E-48//278aa//41%//Q10000

15 C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1 //1.3E-86//522aa//36%//P97998

C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds //0//1770bp//99%//AB023421

C-PLACE1006961

C-PLACE1006962

20 C-PLACE1006966

C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12) //3.2E-35//180aa//33%//Q14542

C-PLACE1007021

C-PLACE1007105

25 C-PLACE1007178

C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) //1E-42//370aa//31%//P54304

C-PLACE1007238

30 C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds //6.5E-216//1068bp//96%//D50495

C-PLACE1007242

C-PLACE1007243//UNC-47 PROTEIN //0.00000017//211aa//27%//P34579

C-PLACE1007257//Homo sapiens mRNA for dia-12c protein //0//2052bp//99%//Y15908

C-PLACE1007274

35 C-PLACE1007282

C-PLACE1007301

C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds //4.1E-17//1037bp//56%//AF117649

C-PLACE1007342

40 C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds //0//2366bp//99%//AF096870

C-PLACE1007367

C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13 //0.00000044//127aa//30%//P27715

45 C-PLACE1007386

C-PLACE1007402

C-PLACE1007409//WHITE PROTEIN //1.1E-64//428aa//32%//Q17320

C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP) //8.8E-25//140aa//35%//P27487

50 C-PLACE1007450

C-PLACE1007452

C-PLACE1007460

C-PLACE1007484

C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR

C-PLACE1007511//KERATIN TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19) //1.4E-85//365aa//45%//P08728

C-PLACE1007511//KERATIN TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19) //1.4E-85//365aa//45%//P08728

- C-PLACE1007524  
 C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164  
 C-PLACE1007544  
 5 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%//P34537  
 C-PLACE1007583  
 C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%//Q99676  
 C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%//AB023194  
 10 C-PLACE1007621  
 C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P32506  
 C-PLACE1007645  
 C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952-bp//99%//AB023194  
 C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.7E-09//279aa//28%//Q26457  
 15 C-PLACE1007690  
 C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%//P43535  
 C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243  
 C-PLACE1007725  
 20 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%//P10265  
 C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%//AB014585  
 C-PLACE1007746  
 C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602  
 25 C-PLACE1007810  
 C-PLACE1007843  
 C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//99%//AP000010  
 C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%//AB018309  
 30 C-PLACE1007897  
 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//25%//Q99323  
 C-PLACE1007954  
 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530  
 35 C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529  
 C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//48%//P52272  
 40 C-PLACE1007990  
 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622  
 C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//1833bp//99%//AC005628  
 45 C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590  
 C-PLACE1008095  
 C-PLACE1008122  
 C-PLACE1008129  
 50 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa//31%//Q09531  
 C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%//P37709  
 C-PLACE1008209  
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA COAT PROTEIN) (GAMMA COAT PROTEIN)  
 C-PLACE1008275//HOMO SAPIENS  
 C-PLACE1008280  
 C-PLACE1008309

- C-PLACE1008329  
 C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%//AB014579  
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%//P05432  
 C-PLACE1008401  
 5 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP)//0//698aa//95%//P41541  
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%//Q06527  
 C-PLACE1008457  
 C-PLACE1008465  
 10 C-PLACE1008488  
 C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine recepto//0//1980bp//99%//AL031778  
 C-PLACE1008531  
 15 C-PLACE1008532  
 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%//P22620  
 C-PLACE1008568  
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%//P37199  
 20 C-PLACE1008621  
 C-PLACE1008626  
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591  
 C-PLACE1008629  
 25 C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//AF044333  
 C-PLACE1008693  
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406  
 30 C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//O35345  
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%//AJ004974  
 C-PLACE1008813  
 35 C-PLACE1008854  
 C-PLACE1008867  
 C-PLACE1008887  
 C-PLACE1008902  
 C-PLACE1008925  
 40 C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623  
 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112  
 C-PLACE1009045  
 C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582  
 C-PLACE1009090  
 45 C-PLACE1009091  
 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%//P30432  
 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%//P51814  
 C-PLACE1009110  
 50 C-PLACE1009111  
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%//Q05086  
 C-PLACE1009158  
 C-PLACE1009166  
 C-PLACE1009187  
 C-PLACE1009190  
 C-PLACE1009230

C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%//AF107295

C-PLACE1009328

C-PLACE1009335

C-PLACE1009338

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%//Q12067

C-PLACE1009375

C-PLACE1009388

C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000047//165aa//73%//Q09820

C-PLACE1009434

C-PLACE1009443

C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%//P42356

C-PLACE1009459

C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%//P54319

C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.9E-40//179aa//37%//P34580

C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%//Q99418

C-PLACE1009542

C-PLACE1009571

C-PLACE1009581

C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%//Q00808

C-PLACE1009607

C-PLACE1009621

C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P25159

C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//1.5E-285//538aa//99%//P55161

C-PLACE1009665

C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534

C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//7E-33//166aa//43%//Q09876

C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200

C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120

C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.3E-294//1329bp//100%//AB012190

C-PLACE1009794

C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%//AB020712

C-PLACE1009886

C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.9E-108//277aa//43%//P53145

C-PLACE1009971

C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-59//450aa//34%//P28175

C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1962bp//99%//AL080122

C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70//736bp//73%//U48288

C-PLACE1010023

C-PLACE1010031

C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%//X84692

C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482

C-PLACE1010076

C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44%//Q04652

C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//

99%/AL049385

C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%/P22082

5 C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%/P35662

C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%/Q01130

C-PLACE1010202

C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%/P25722

10 C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%/AL080122

C-PLACE1010293

C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.1E-09//350aa//22%/P52178

15 C-PLACE1010324

C-PLACE1010329

C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.00000002//126aa//29%/P34024

C-PLACE1010364

20 C-PLACE1010383

C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%/AB020643

C-PLACE1010491

C-PLACE1010492

25 C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%/AB022718

C-PLACE1010529

C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%/P253 86

30 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%/AB017546

C-PLACE1010616

C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%/P02642

C-PLACE1010629

C-PLACE1010630

35 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%/Q01755

C-PLACE1010714

C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299//1091bp//99%/AB019987

40 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%/AF020267

C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%/X68061

C-PLACE1010786

C-PLACE1010800

C-PLACE1010811

45 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%/Q05481

C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%/AB011182

C-PLACE1010900

C-PLACE2000050

50 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.4E-191//828aa//48%/P21783

C-PLACE4000590

C-PLACE4000638

C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS PROTEIN) (TSC2)

## Homology Search Result Data 7.

[0315] The result of the homology search of the SwissProt using the 5'-end sequence (54 clones selected in EXAM-  
 PLE 16).

5 [0316] Data include

the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 10 the organism and the Accession No. of the top hit data, as in the order separated by //.

[0317] Data are not shown for the clones in which the P-value was higher than 1.

15 F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)//0.13//52//38//P25860  
 F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 64E)//2.2e-28//104//59//Q24574  
 F-HEMBA1003854//VERPROLIN//0.012//138//31//P37370  
 20 F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT)//0.93//39//  
 33//Q37131  
 F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2)//0.90//20//50//P38524  
 F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16)//7.6e-46//141//58//Q15973  
 F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT)//0.0033//32//46//P70560  
 F-HEMBA1006092//VERPROLIN//1.0//62//35//P37370  
 25 F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10)//0.30//41//36//P12350  
 F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR//0.089//21//52//Q02593  
 F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY)//0.38//156//30//P28697  
 F-HEMBB1000672  
 F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65)//1.0//30//36//P16012  
 30 F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1)//3.7e-54//  
 241//47//P47853  
 F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3'REGION (ORF3)//0.59//48//39//Q51483  
 F-MAMMA1002094  
 F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.26//58//27//P06333  
 35 F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)//8.9e-20//83//48//P10895  
 F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT)//1.0//42//40//P19326  
 F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR (ALS)//6.0e-23//207//32//Q02833  
 40 F-NT2RM4001178//HOMEBOX PROTEIN OTX3 (ZOTX3)//0.012//156//28//Q90267  
 F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//0.0012//81//37//P13816  
 F-NT2RP2000198//CREB-BINDING PROTEIN//0.29//98//37//Q92793  
 F-NT2RP2000551//PROTEIN Q300//0.00017//23//60//Q02722  
 F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401//1.0//41//29//Q57844  
 45 F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC//0.27//13//61//Q01644  
 F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-)//0.089//99//29//Q99014  
 F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)//4.0e-13//177//  
 28//P16372  
 F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI2 5'REGION//0.37//12//75//P53820  
 50 F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)//0.99//61//32//Q42616  
 F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2//3.3e-10//90//35//Q06666  
 F-NT2RP2002843//CYTOCHROME B//0.78//103//26//P48884  
 F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG//0.40//28//46//P37209  
 F-NT2RP2003799//HYPOTHETICAL PROTEIN M10116.1//0.80//55//32//P81303  
 F-NT2RP2004420  
 F-NT2RP2004920//HISTIDINE-RICH METAL BINDING POLYPEPTIDE//0.18//18//55//Q48251  
 F-NT2RP2005454

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT)//7.4e-38//136//41//P51003  
 F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//4.0e-08//180//28//P32323  
 F-NT2RP2005882  
 5 F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB//0.0022//69//39//P39217  
 F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)//0.00035//127//31//P15276  
 F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.97//71//28//P05204  
 F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT)//0.064//110//34//P39881  
 10 F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.020//95//29//P15583  
 F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.8e-05//165//29//P17437  
 15 F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.035//152//30//P10162  
 F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN)//0.38//124//31//P28284  
 F-OVARC1001029  
 20 F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.45//61//24//Q42377  
 F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29)//0.70//121//32//P47845  
 F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1)//3.2e-08//205//24//P53046  
 25 F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210)//0.99//52//38//P01668

## Homology Search Result Data 8.

30 **[0318]** The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

**[0319]** Data include

the name of clone,  
 35 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

**[0320]** Data are not shown for the clones in which the P-value was higher than 1.

40 F-HEMBA1000497  
 F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs//6.6e-101//473//99//V00710  
 F-HEMBA1003854//Homo sapiens clone RG270D13, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 18 unordered pieces//1.7e-05//412//61//AC005081  
 45 F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence//0.77//466//59//AC002386  
 F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds//6.7e-07//492//57//U29953  
 F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt]//2.9e-47//341//77//S54641  
 50 F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence//0.28//436//59//Z83851  
 F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence//0.28//309//60//U95738  
 F-HEMBA1006406//HS 2268 B2 C07 MR CIT Approved Human Genomic Sperm Library D. Ham  
 F-HEMBA1006650//H sapiens, Caucasian, NA genomic MspI fragment, 1.0 kb, forward read, coding  
 4e-24//143//96//Z55730  
 F-HEMBA1006812//X.laevis xUBFa1phal mRNA for upstream binding factor 2//0.96//234//64//X59863

F-HEM BB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158

F-HEM BB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760

5 F-HEM BB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127

F-MAMMA1001252

F-MAMMA1002094//H.sapiens CpG island DNA genomic MseI fragment, clone 184g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993

10 F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136

F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108

F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199

15 F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961

F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411

F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//0.00013//121//76//AC005670

20 F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827

F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812

F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622

F-NT2RP2001214

25 F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189

F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589

F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094

30 F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 1 ordered pieces.//0.032//141//70//AC006097

F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.7/1.8e-22//377//69//AP000018

35 F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050

F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476

F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233

40 F-NT2RP2004095//HS\_3083\_A1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698

F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035

F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970

45 F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410

F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770

F-NT2RP2005806//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652

50 F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242

F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775

F-NT2RP3001723//H.sapiens CpG island DNA genomic MseI fragment, clone 13g5, reverse read cpg13g5.rt1a.//2.2e-18//163//85//Z56771

F-NT2RP3001723

U00518

NT2RP3003155

F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//I40055

F-OVARC1000008///0.0040//674//57//M82836

F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4) //1.1e-07//519//59//X06461

F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221

F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769

F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427

F-PLACE1003030

F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081

F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//3.1e-39//214//98//AL031660

#### Homology Search Result Data 9.

[0321] The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0322] Data include

the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

[0323] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0324] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.4e-38//185//84//U14567  
R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785

R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, STSs, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL031281

R-HEMBA1004193//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-34//188//81//U14567  
R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC004241

R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence.//3.1e-21//341//67//AJ010598

R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//1.7e-24//307//71//AC004678

R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase.//0.76//246//62//X63282

R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.3e-31//297//77//AL023574

R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.8e-15//350//65//AC003071

R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.8e-55//430//81//Z82207

R-HEMBA100672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence.//9.1e-39//437//71//AC006166

R-HEMBA1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.5e-37//275//85//AC004593

R-HEMBA1001871//Plasmodium falciparum chromosome 12 clone 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//0.00027//410//59//AC004688

R-MAMMA1002094//Homo sapiens clone 3163, A1 A09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1-6e-21//283//73//AC005258  
 R-NT2RM4000657  
 R-NT2RM4000783  
 5 R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073  
 R-NT2RM4001178  
 R-NT2RM4002420  
 10 R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence, complete sequence.//0.58//108//67//AC002307  
 R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//D30043  
 R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//0.0058//166//69//AC005324  
 15 R-NT2RF2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822  
 R-NT2RP2001460  
 R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228  
 20 R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181  
 R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168  
 R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X \*.//5.3e-39//449//72//Z81014  
 25 R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0.0097//498//59//AC005412  
 R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey sequence.//1.2e-32//344//75//AQ196754  
 30 R-NT2RP2003799//3.6e-05//408//60//AL010237  
 R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//2.1e-10//455//61//AL034557  
 R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence.//5.1e-51//383//74//AL031287  
 35 R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence.//0.062//315//61//AC005219  
 R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindDIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//0.75//246//63//Z86062  
 40 R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence.//0.91//232//61//AC005232  
 R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence.//1.3e-19//405//66//U37368  
 R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-09//533//60//Z97348  
 45 R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.00026//499//58//AL034560  
 R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence.//0.00035//337//61//AC002466  
 R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.8e-44//307//86//AC005180  
 R-NT2RP3003155  
 50 R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence.//0.95//95//65//B21351  
 R-OVARC1000008  
 R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.91//83//71//AC005161  
 R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//1.2e-09//165//75//AC002357

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//75//AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387

5 R-PLACE10e5549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence.//0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.1e-88//497//91//AL031660

10 Homology Search Result Data 10.

**[0325]** The result of the homology search of the Human Unigene using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) .

**[0326]** Data include

15

the name of clone,  
title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

20

**[0327]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//ou15a11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1626332 3', mRNA sequence.//1.0//186//65//AI018130

25

F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element; mRNA sequence.//3.7e-06//140//70//AA749151

30

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//AB000732

35

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element; mRNA sequence.//0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:002710 002710 GAG POLYPROTEIN ; mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087

40

F-HEMBA1006812//zh49f01.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:415417 3', mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBA1000672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBA1001197//tq45e03.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:001940 001940 STRAWBERRY NOTCH ; mRNA sequence.//1.2e-16//117//92//AI580023

45

F-HEMBA1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

50

F-NT2RM4000634//DKFZp434D1813\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence.//1.8e-20//470//65//AI703299

F-NT2RM4000857//Homo sapiens KIAA0116 mRNA, partial cds.//1.2e-120//579//98//W80404

F-NT2RM4000857//Homo sapiens KIAA0116 mRNA, partial cds.//1.2e-120//579//98//W80404

F-NT2RM4000857//Homo sapiens KIAA0116 mRNA, partial cds.//1.2e-120//579//98//W80404

F-NT2RM4002420//wg39f11.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:2367501 3' similar to contains element L1 L1 repetitive element; mRNA sequence.//1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997  
 F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence.//5.0e-07//116//71//AA017066  
 F-NT2RP2000660//qx01g11.x1 NCI\_CGAP\_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence.//0.027//120//65//AI225283  
 F-NT2RP2001214  
 F-NT2RP2001460//wb50h10.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence.//0.0013//89//78//AI651878  
 F-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//2.3e-18//120//93//AA427992  
 F-NT2RP2002056//tw44g09.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element; mRNA sequence.//2.4e-07//99//79//AI811687  
 F-NT2RP2002677  
 F-NT2RP2002755//zj83d10.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:461491 3' similar to contains element TAR1 repetitive element ; mRNA sequence.//1.9e-19//229//76//AA705059  
 F-NT2RP2002843//wt88d12.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR: P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN.; mRNA sequence.//8.2e-15//314//67//AI964055  
 F-NT2RP2003101//wi65a03.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence.//0.38//106//68//AI763133  
 F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979  
 F-NT2HP2004095  
 F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691  
 F-NT2RP2004920//wz68d10.x1 NCI\_CGAP\_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR: 000172 000172 LINE-1 REVERSE TRANSCRIPTASE ; mRNA sequence.//0.0020//220//61//AI969546  
 F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194  
 F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770  
 F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mRNA sequence.//2.0e-05//385//62//Z78328  
 F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362  
 F-NT2RP3001282  
 F-NT2RP3001723//ws73d05.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSR1.t1 TAR1 TAR1 repetitive element ; mRNA sequence.//2.6e-07//245//66//AW008782  
 F-NT2RP3002099//yg49d01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence.//0.58//164//64//R46086  
 F-NT2RP3003155  
 F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997  
 F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565  
 F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541  
 F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802  
 F-OVARC1001029//qv29c05.x1 NCI\_CGAP\_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element ; mRNA sequence.//0.0012//145//68//AI252422  
 F-PLACE1000814//ak42f05.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence.//7.1e-31//275//76//AA868469  
 F-PLACE1003030  
 F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//1.2e-57//737//67//AJ010046  
 F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence.//2.2e-21//216//76//H52716

Homology Search Result Data 11.

[0328] The result of the homology search of the Human Unigene using the clone sequence of 3' end (54 clones

Accession: F-NT2RP2000198

329 3' end (54 clones)

the name of clone.

title of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

- 5 [0330] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.  
[0331] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//np09h02.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains  
Alu repetitive element;contains element MER22 repetitive element ; mRNA sequence.//6.2e-38//185//83//  
10 AA614254  
R-HEMBA1001750//yy71b10.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:  
278971 3', mRNA sequence.//0.004511193//63//N63303  
R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133)//3.4e-72//310//  
80//AL049263  
15 R-HEMBA1004193//tr01e08.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to con-  
tains Alu repetitive element;contains element MER4 repetitive element ; mRNA sequence.//1.5e-33//186//81//  
AI914747  
R-HEMBA1004860//qh16b06.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA  
sequence.//0.017//118//69//AI218308  
20 R-HEMBA1005572//wj16h05.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA se-  
quence.//4.6e-111//522//99//AI861830  
R-HEMBA1006038//DKFZp434E1117\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5',  
mRNA sequence.//1.2e-22//295//72//AL041450  
R-HEMBA1006092//qt30d09.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE: 1949489  
25 3' similar to contains element PTR5 repetitive element ; mRNA sequence.//1.4e-87//422//98//AI337963  
R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291-//76//AB018295  
R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630  
R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087  
R-HEMBA100672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011)//3.2e-48//276//  
30 74//AL096734  
R-HEMBA1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar  
to contains Alu repetitive element; mRNA sequence.//9.9e-44//275//88//AA410788  
R-HEMBA1001871//wg20c02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321  
35 R-MAMMA1001252//aa61h04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to con-  
tains Alu repetitive element;contains element XTR repetitive element ; mRNA sequence.//9.0e-19//127//91//  
AA504355  
R-MAMMA1002094//wd28h12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mR-  
NA sequence.//2.5e-68//328//99//AI936520  
40 R-NT2RM4000634//DKFZp434F2016\_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3',  
mRNA sequence.//8.2e-20//185//81//AL041146  
R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992  
R-NT2RM4000783  
R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136  
45 R-NT2RM4001178//tk08e03.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA se-  
quence.//0.77//96//62//AI457506  
R-NT2RM4002420//wl58b04.x1 NCI\_CGAP\_Bm25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA se-  
quence.//2.4e-85//438//94//AI857508  
R-NT2RP2000198//nx19b11.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA se-  
50 quence.//1.9e-45//270//91//AA738352  
R-NT2RP2000551//tg80h11.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA se-  
quence.//3.3e-53//311//85//AI417680  
R-NT2RP2000660//ns42a06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA se-  
quence.//4.3e-26//142//97//AA805691  
R-NT2RP2001460  
R-NT2RP2001460  
R-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3'

similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence //6.0e-13//85//96//AA427992  
R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130846 3', mRNA  
sequence //0.0016//208//65//R22302

R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096

5 R-NT2RP2002755//qd50d10.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone IMAGE:1732915 3',  
mRNA sequence //1.5e-26//419//66//AI190698

R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373639 3' similar to  
contains L1.t1 L1 repetitive element; mRNA sequence //1.8e-45//463//74//AI749673

10 R-NT2RP2003101//ty24h05.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA se-  
quence //7.5e-73//347//99//AI758824

R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294

R-NT2RP2004095//zv08c02.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to con-  
tains element MER32 repetitive element ; mRNA sequence //9.6e-07//188//66//AA436455

15 R-NT2RP2004732//tu60a07.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to con-  
tains Alu repetitive element; contains element L1 repetitive element ; mRNA sequence //4.3e-25//414//68//  
AI678956

R-NT2RP2004920//wd13h02.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA se-  
quence //6.8e-91//483//93//AI694022

20 R-NT2RP2005454//yy77g09.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE:  
279616 3', mRNA sequence //0.0070//325//59//N48302

R-NT2RP2005776//qq97d06.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:1939307 3',  
mRNA sequence //7.5e-08//89//82//AI338419

R-NT2RP2005806//wc29h01.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to con-  
tains MER2.b3 MER2 repetitive element ; mRNA sequence //3.2e-16//235//71//AI671398

25 R-NT2RP2005882//wo31f09.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA se-  
quence //0.00095//352//59//AI925528

R-NT2RP3001282//wg35b03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE:  
2367053 3', mRNA sequence //1.7e-113//555//97//AI769199

30 R-NT2RP3001723//wo48e06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA se-  
quence //4.2e-98//471//98//AI926617

R-NT2RP3002099//DKFZp564L227\_s1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564L227 3', mR-  
NA sequence //9.2e-50//329//87//AL037910

R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668  
3', mRNA sequence //1.4e-30//159//99//AA173172

35 R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035594

R-OVARC1000008//wa69e12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA  
sequence //1.0e-77//376//98//AI699393

R-OVARC1000724//tf94b10.x1 NCI\_CGAP\_CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA se-  
quence //0.71//27//100//AI380236

40 R-OVARC1000751//og93d04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA se-  
quence //3.5e-13//274//63//AA863306

R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar  
to contains Alu repetitive element; contains element PTR5 repetitive element ; mRNA sequence //3.5e-13//175//74//  
N99464

45 R-PLACE1000814//tg49a08.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar  
to contains L1.t2 L1 L1 repetitive element; mRNA sequence //2.2e-18//285//69//AI424789

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
cds //4.0e-34//225//90//AF032387

50 R-PLACE1005549//tm26b11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA  
sequence //0.91//127//66//AI480253

R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5'  
similar to contains Alu repetitive element; contains LTR4 repetitive element; mRNA sequence //2.4e-36//245//87//  
R92256

and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

- C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS)//6.4E-99//457aa//45%//Q09996
- 5 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344
- C-HEMBA1000129//HYTOTHEICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//Q09884
- C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B)//0//1612bp//99%//AJ011738
- 10 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%//Q61221
- C-HEMBA1000231
- C-HEMBA1000264
- C-HEMBA1000280
- C-HEMBA1000282
- 15 C-HEMBA1000303//&quot;Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.&quot;//7.1E-254//1440bp//87%//AF030131
- C-HEMBA1000333//&quot;Homo sapiens mRNA for KIAA0874 protein, partial cds.&quot;//4.8E-253//1148bp//99%//AB020681
- C-HEMBA1000351
- 20 C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp566C243).//3.3E-287//815bp//98%//AL050274
- C-HEMBA1000396
- C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357
- C-HEMBA1000442
- 25 C-HEMBA1000456
- C-HEMBA1000504
- C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490
- C-HEMBA1000519
- C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01755
- 30 C-HEMBA1000542//&quot;Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.&quot;//2.2E-194//663bp//83%//D89340
- C-HEMBA1000545
- C-HEMBA1000557
- C-HEMBA1000592//&quot;Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.&quot;//0//1465bp//99%//AF121856
- 35 C-HEMBA1000594
- C-HEMBA1000604
- C-HEMBA1000622
- C-HEMBA1000637
- 40 C-HEMBA1000655
- C-HEMBA1000657//&quot;Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.&quot;//7.2E-156//1366bp//76%//U35776
- C-HEMBA1000749
- C-HEMBA1000769
- 45 C-HEMBA1000773
- C-HEMBA1000774
- C-HEMBA1000822
- C-HEMBA1000843
- C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%//P51689
- 50 C-HEMBA1000870
- C-HEMBA1000908
- C-HEMBA1000934
- C-HEMBA1000972
- C-HEMBA1000988
- C-HEMBA1000989
- C-HEMBA1001059//&quot;Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14 &quot;//4.8E-169//786bp//99%//U06088

C-HEMBA1001094

C-HEMBA1001302//&quot;Homo sapiens calcium binding protein precursor, mRNA, complete cds.&quot;//9.6E-258/682bp/94%//AF153686

C-HEMBA1001330

C-HEMBA1001497

C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2)//2.3E-53/110aa//100%//P19065

C-HEMBA1001570

C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS)//1.6E-166//506aa//60%//P42803

C-HEMBA1001640

C-HEMBA1001655

C-HEMBA1001672//&quot;Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.&quot;//0//1707bp//98%//AF072247

C-HEMBA1001711

C-HEMBA1001723//&quot;Rattus norvegicus G beta-like protein GBL mRNA, complete cds.&quot;//4.7E-172//1240bp//81%//AF051155

C-HEMBA1001746//&quot;Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.&quot;//7.6E-59/998bp//64%/AF098066

C-HEMBA1001781

C-HEMBA1001804//&quot;Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.  
&quot;//0//1637bp//99%//AF125158

C-HEMBA1001822//&quot;Mus musculus Ese2L protein mRNA, complete cds.&quot;//1.9E-235//1329bp//89%//  
AF132479

C-HEMBA1001824

C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
(DUGT)//5.7E-51//234aa//41%//Q09332

C-HEMBA1001910

C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535

C-HEMBA1001921//&quot;Homo sapiens germinal center related protein kinase mRNA, complete cds.  
&quot;//0/1850bp/99%//AF000145

C-HEMBA1001939

C-HEMBA1001950//&quot;Homo sapiens mRNA for KIAA0971 protein, complete cds.&quot;//0//1974bp//99%//  
AB023188

C-HEMBA1001967//&quot;Homo sapiens NY-REN-57 antigen mRNA, partial cds.&quot;://0//1721bp//99%//  
AF155114

C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%//AL050089

C-HEMBA1002092//&quot;Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.  
&quot;//1.3E-271//1583bp//88%//U92703

C-HEMBA1002102//ANKYRIN./4.40E-10//106aa//35%//Q02357

C-HEMBA1002150

C-HEMBA1002151//&quot;Rattus norvegicus p34 mRNA, complete cds.&quot;//1.1E-153//1059bp//82%//AF178669

C-HEMBA1002189

C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226

C-HEMBA1002229

C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087

C-HEMBA1002341//&quot;Homo sapiens mRNA for KIAA0771 protein, partial cds.&quot;//0//1514bp//99%//  
AB018314

C-HEMBA1002417//&quot;Homo sapiens chromosome 19, cosmid R28784, complete sequence.&quot;//1.4E-299//294bp//100%//AC005954

HEMBA10025478

MBA

EMBA 100000

HEMBA1002816

C-HEMBA1002970

C-HEMBA1002999//&quot;Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.  
&quot;//1.4E-171//1552bp//75%//U20286

C-HEMBA1003021

C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%//P24014

5 C-HEMBA1003079

C-HEMBA1003273

C-HEMBA1003304

C-HEMBA1003309

C-HEMBA1003376

10 C-HEMBA1003384

C-HEMBA1003531

C-HEMBA1003548

C-HEMBA1003556

C-HEMBA1003571

15 C-HEMBA1003579

C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//32%//Q13105

C-HEMBA1003692

C-HEMBA1003720

C-HEMBA1003725

20 C-HEMBA1003729

C-HEMBA1003758

C-HEMBA1003773//&quot;Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.  
&quot;//5.8E-81//511bp//86%//U17343

C-HEMBA1003783//&quot;Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.&quot;//  
25 1.1E-190//1204bp//84%//AF084259

C-HEMBA1003799

C-HEMBA1003804

C-HEMBA1003805//&quot;Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.&quot;//  
0//988bp//95%//AF090402

30 C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484

C-HEMBA1003856

C-HEMBA1003866//&quot;Mus musculus semaphorin VIa mRNA, complete cds.&quot;//1.2E-105//1192bp//70%//  
AF030430

C-HEMBA1003879

35 C-HEMBA1003880

C-HEMBA1003893

C-HEMBA1003908

C-HEMBA1003937

C-HEMBA1003942

40 C-HEMBA1003958

C-HEMBA1003976

C-HEMBA1003978//&quot;Homo sapiens mRNA for KIAA0840 protein, partial cds.&quot;//0//1530bp//100%//  
AB020647

C-HEMBA1003985

45 C-HEMBA1004011

C-HEMBA1004024

C-HEMBA1004038

C-HEMBA1004045

C-HEMBA1004048

50 C-HEMBA1004111//&quot;Homo sapiens mRNA for KIAA1276 protein, partial cds.&quot;//1.00E-163//751bp//  
99%//AB033102

C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q14141

C-HEMBA1004138

C-HEMBA1004143

C-HEMBA1004148

C-HEMBA1004155//&quot;Homo sapiens mRNA for KIAA1276 protein, partial cds.&quot;//1.00E-163//751bp//  
99%//AB033102

C-HEMBA1004200

C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13//6.2E-30//208aa//37%//P51153

C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2//1.5E-12//258aa//29%//P40991

C-HEMBA1004238

C-HEMBA1004248//"Homo sapiens insulin induced protein 2 mRNA, complete cds."//8.20E-175//552bp//97%//AF125392

C-HEMBA1004272

C-HEMBA1004274

C-HEMBA1004275//"Homo sapiens mRNA for KIAA1111 protein, partial cds."//0//1341bp//99%//AB029034

C-HEMBA1004286//"Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds."//0//1982bp//99%//AF022795

C-HEMBA1004312

C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT)//2.3E-93//357aa//42%//Q99676

C-HEMBA1004323

C-HEMBA1004327

C-HEMBA1004330

C-HEMBA1004341

C-HEMBA1004366

C-HEMBA1004372

C-HEMBA1004389//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//1437bp//99%//AF125158

C-HEMBA1004394

C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10)//3.2E-32//148aa//52%//P52017

C-HEMBA1004429

C-HEMBA1004460

C-HEMBA1004461

C-HEMBA1004502

C-HEMBA1004554

C-HEMBA1004560

C-HEMBA1004610

C-HEMBA1004629

C-HEMBA1004632

C-HEMBA1004637

C-HEMBA1004670

C-HEMBA1004672

C-HEMBA1004697

C-HEMBA1004711

C-HEMBA1004725

C-HEMBA1004730

C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)//9.9E-39//143aa//52%//P42743

C-HEMBA1004751

C-HEMBA1004752

C-HEMBA1004889//"Human C3f mRNA, complete cds."//6.70E-24//341aa//26%//U72515

C-HEMBA1004934

C-HEMBA1004944

C-HEMBA1004973

C-HEMBA1004977

C-HEMBA1005009//"Homo sapiens BAF53a (BAF53a) mRNA, complete cds."//0//1813bp//99%//AF041474

C-HEMBA1005083

C-HEMBA1005113

C-HEMBA1005133

C-HEMBA1005194

C-HEMBA1005219//"Homo sapiens mRNA for KIAA0585 protein, partial cds."//1.2E-268//1215bp//99%//AB011157

C-HEMBA1005252//"Homo sapiens mRNA for KIAA0585 protein, partial cds."//1.2E-268//1215bp//99%//AB011157

C-HEMBA1005296  
 C-HEMBA1005314  
 C-HEMBA1005331  
 C-HEMBA1005394  
 5 C-HEMBA1005403  
 C-HEMBA1005423//&quot;Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.  
 &quot;//2E-213//537bp//99%//AF041248  
 C-HEMBA1005468  
 C-HEMBA1005469  
 10 C-HEMBA1005474  
 C-HEMBA1005517  
 C-HEMBA1005518  
 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1)//3.1E-154//285aa//99%//Q60809  
 C-HEMBA1005558//NUCLEAR PROTEIN SNF7//6.40E-16//170aa//31%//P39929  
 15 C-HEMBA1005576//&quot;Homo sapiens mRNA for KIAA0463 protein, partial cds.&quot;//1.1E-181//835bp//  
 99%//AB007932  
 C-HEMBA1005582//&quot;TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL  
 TROPOMYOSIN).&quot;//0.00000009//213aa//27%//P09492  
 C-HEMBA1005583  
 20 C-HEMBA1005595//&quot;DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).&quot;//2.3E-54//562aa//29%//P34036  
 C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133).//2.2e-315//  
 1448bp//99%//AI 050012  
 C-HEMBA1005621//&quot;Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds.&quot;//2.9E-224//  
 1031bp//99%//AF139365  
 25 C-HEMBA1005666  
 C-HEMBA1005680  
 C-HEMBA1005685  
 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT)//  
 4.4E-17//167aa//34%//P25296  
 30 C-HEMBA1005746  
 C-HEMBA1005755  
 C-HEMBA1005813  
 C-HEMBA1005822  
 C-HEMBA1005834  
 35 C-HEMBA1005884  
 C-HEMBA1005891  
 C-HEMBA1005909  
 C-HEMBA1005911  
 C-HEMBA1005931  
 40 C-HEMBA1005963  
 C-HEMBA1005991  
 C-HEMBA1006005  
 C-HEMBA1006031//&quot;Homo sapiens mRNA for putative phospholipase, complete cds.&quot;//0//1413bp//  
 99%//AB019435  
 45 C-HEMBA1006067  
 C-HEMBA1006081  
 C-HEMBA1006091  
 C-HEMBA1006100  
 C-HEMBA1006108//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//4.8E-245//764bp//  
 99%//AB023160  
 50 C-HEMBA1006121  
 C-HEMBA1006130//SEL-10 PROTEIN//0.000000043//219aa//25%//Q93794  
 C-HEMBA1006155  
 C-HEMBA1006158//&quot;Homo sapiens transcription factor forkhead box P3 (FKBP3) mRNA, complete cds.  
 &quot;//1.1E-181//835bp//99%//AB007932  
 C-HEMBA1006181  
 C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR//1.9E-19//215aa//39%//P05142  
 C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//0//1615bp//99%//AF070557

- C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR//0.00000002//62aa//53%//P42698  
C-HEMBA1006259
- 5 C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-)//1.3E-123//200aa//73%//P10265  
C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//1E-210//490aa//77%//P25500  
C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2//0.000000012//176aa//30%//P32505  
C-HEMBA1006284
- 10 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-)//4.2E-12//215aa//23%//P70473  
C-HEMBA1006293  
C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//1.4E-48//248aa//43%//P38821  
C-HEMBA1006349
- 15 C-HEMBA1006364  
C-HEMBA1006381  
C-HEMBA1006398//"Human L1 element L1.6 putative p150 gene, complete cds."//2E-277//1729bp//85%//U93563  
C-HEMBA1006445//"Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds."//1.4E-270//1224bp//100%//U96750
- 20 C-HEMBA1006483  
C-HEMBA1006492  
C-HEMBA1006497  
C-HEMBA1006502
- 25 C-HEMBA1006507//"Homo sapiens mRNA for KIAA0666 protein, partial cds."//0//2334bp//99%//AB014566  
C-HEMBA1006535  
C-HEMBA1006559//"Mus musculus PRAJA1 (Praj1) mRNA, complete cds."//2.8E-206//1107bp//83%//U06944
- 30 C-HEMBA1006566  
C-HEMBA1006579  
C-HEMBA1006583  
C-HEMBA1006612  
C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG//0.00000069//109aa//38%//Q58323
- 35 C-HEMBA1006643  
C-HEMBA1006674  
C-HEMBA1006682  
C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION//3.3E-22//241aa//31%//P53196  
C-HEMBA1006717  
C-HEMBA1006744  
C-HEMBA1006754  
C-HEMBA1006767
- 45 C-HEMBA1006789  
C-HEMBA1006832  
C-HEMBA1006885//"Homo sapiens gene for Proline synthetase associated, complete cds."//0//1467bp//96%//AB018566  
C-HEMBA1006900
- 50 C-HEMBA1006926  
C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//1.8E-226//1039bp//99%//AJ010841  
C-HEMBA1006973//"Homo sapiens rab3-GAP regulatory domain mRNA, complete cds."//5.6E-143//740bp//94%//AF004828  
C-HEMBA1007001  
C-HEMBA1007062  
C-HEMBA1007080

C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626

C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//99%//AL117450

C-HEMBA1007194//&quot;Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.&quot;//0//1588bp//99%//AF139658

C-HEMBA1007206

C-HEMBA1007256

C-HEMBA1007267

C-HEMBA1007281

C-HEMBA1007300//&quot;Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds.&quot;//0//1519bp//99%//AF127479

C-HEMBA1007301

C-HEMBA1007319

C-HEMBA1007320

C-HEMBA1007327

C-HEMBA1007347

C-HEMBA1000005

C-HEMBA1000030

C-HEMBA1000048

C-HEMBA1000099

C-HEMBA1000141

C-HEMBA1000198

C-HEMBA1000217//&quot;Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.&quot;//0//1038bp//99%//AF090385

C-HEMBA1000218

C-HEMBA1000274

C-HEMBA1000312

C-HEMBA1000402

C-HEMBA1000420

C-HEMBA1000480

C-HEMBA1000530

C-HEMBA1000550

C-HEMBA1000556//&quot;Homo sapiens mRNA for KIAA0750 protein, complete cds.&quot;//6.3E-74//1213bp//64%//AB018293

C-HEMBA1000586

C-HEMBA1000592

C-HEMBA1000593//&quot;Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.&quot;//1.3E-107//503bp//99%//AF067864

C-HEMBA1000649

C-HEMBA1000693//&quot;Homo sapiens neuroan1 mRNA, complete cds.&quot;//0//2952bp//94%//AF040723

C-HEMBA1000822

C-HEMBA1000826

C-HEMBA1000890

C-HEMBA1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122

C-HEMBA1001008

C-HEMBA1001020//&quot;Homo sapiens mRNA for KIAA0889 protein, complete cds.&quot;//0//1812bp//98%//AB020696

C-HEMBA1001051

C-HEMBA1001112//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//6E-145//961bp//83%//AF077032

C-HEMBA1001221

C-HEMBA1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//54%//P46938

C-HEMBA1001282//ANKYRIN R (ANKYRINS 2 1 AND 2 2) (ERYTHROCYTE ANKYRIN).//7E-43//394aa//92%//AF0157

C-HEMBA1001300

C-HEMBA1001301

C-HEMBA1001337

C-HEM BB1001356  
 C-HEM BB1001364  
 C-HEM BB1001366  
 C-HEM BB1001367  
 5 C-HEM BB1001527  
 C-HEM BB1001537  
 C-HEM BB1002359  
 C-HEM BB1002415  
 C-HEM BB1002457  
 10 C-HEM BB1002492  
 C-HEM BB1002495  
 C-HEM BB1002502  
 C-HEM BB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%//P27544  
 C-HEM BB1002600//&quot;Homo sapiens tetraspan NET-5 mRNA, complete cds.&quot;//0//1417bp//99%//  
 15 AF089749  
 C-HEM BB1002607//&quot;Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.  
 &quot;//2E-136//660bp//98%//AF105421  
 C-HEM BB1002684  
 C-HEM BB1002692  
 20 C-HEM BB1002697  
 C-HEM BB1002705//&quot;Homo sapiens CGI-27 protein mRNA, complete cds.&quot;//7.80E-285//841bp//96%//  
 AF132961  
 C-MAMMA1000019  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.2E-198//868bp//99%//  
 25 Z47553  
 C-MAMMA1000025  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//323aa//48%//P47226  
 C-MAMMA1000069  
 C-MAMMA1000084  
 30 C-MAMMA1000139  
 C-MAMMA1000163  
 C-MAMMA1000171  
 C-MAMMA1000173//&quot;Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete  
 cds.&quot;//2.6E-164//1044bp//87%//AF197060  
 35 C-MAMMA1000277  
 C-MAMMA1000278  
 C-MAMMA1000284//P.walti mRNA for mp associated protein 55.//2.2E-109//864bp//76%//X99836  
 C-MAMMA1000309  
 C-MAMMA1000312  
 40 C-MAMMA1000313  
 C-MAMMA1000361  
 C-MAMMA1000388//&quot;Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.&quot;//  
 0//1466bp//99%//AB015132  
 C-MAMMA1000395  
 45 C-MAMMA1000410  
 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//  
 53%//Q09232  
 C-MAMMA1000421  
 C-MAMMA1000422  
 50 C-MAMMA1000468  
 C-MAMMA1000472  
 C-MAMMA1000490  
 C-MAMMA1000524  
 C-MAMMA1000567  
 C-MAMMA1000568  
 C-MAMMA1000569  
 C-MAMMA1000570  
 C-MAMMA1000571  
 C-MAMMA1000572  
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 C-MAMMA1000619  
 C-MAMMA1000620  
 C-MAMMA1000621  
 C-MAMMA1000622  
 C-MAMMA1000623  
 C-MAMMA1000624  
 C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%//P48365

- C-MAMMA1000664  
 C-MAMMA1000670  
 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//4.4E-33//250aa//33%//P42660
- 5 C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16)//7.70E-17//246aa//29%//P94524  
 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//1E-77//395aa//45%//014646  
 C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein//0//1587bp//99%//AJ011779  
 C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I//9E-299//1033aa//55%//P87115
- 10 C-MAMMA1000746  
 C-MAMMA1000775  
 C-MAMMA1000824//ACTIN//6.2E-20//284aa//28%//P53500  
 C-MAMMA1000831
- 15 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4)//7.8E-40//101aa//54%//027540  
 C-MAMMA1000842  
 C-MAMMA1000843  
 C-MAMMA1000856  
 C-MAMMA1000865
- 20 C-MAMMA1000875  
 C-MAMMA1000906  
 C-MAMMA1000908  
 C-MAMMA1000914
- 25 C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8//0//1767bp//99%//AJ250711  
 C-MAMMA1000968  
 C-MAMMA1000979  
 C-MAMMA1001008//"Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//1263bp//99%//AF117892  
 C-MAMMA1001021
- 30 C-MAMMA1001041//"SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1)."//1.6E-16//113aa//41%//Q01082  
 C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5//0//1440bp//99%//AJ237946  
 C-MAMMA1001075//"Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-181//397bp//98%//AF151830
- 35 C-MAMMA1001078  
 C-MAMMA1001091  
 C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN)//4E-49//125aa//68%//P51521  
 C-MAMMA1001110  
 C-MAMMA1001126
- 40 C-MAMMA1001139//SRE-2 PROTEIN//5.80E-35//239aa//38%//Q09273  
 C-MAMMA1001143  
 C-MAMMA1001154  
 C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR//1.30E-07//81aa//45%//Q92338  
 C-MAMMA1001215
- 45 C-MAMMA1001244  
 C-MAMMA1001259//"Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//89%//AF184275  
 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III//2.1E-52//630aa//30%//P34537
- 50 C-MAMMA1001343  
 C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823)//0//2131bp//99%//AL080121  
 C-MAMMA1001419  
 C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT OF UTP-DEPENDENT URIDINE KINASE)  
 C-MAMMA1001552  
 C-MAMMA1001552  
 C-MAMMA1001576//"Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%//

M61764

C-MAMMA1001604

C-MAMMA1001620

C-MAMMA1001635

5 C-MAMMA1001649

C-MAMMA1001686

C-MAMMA1001692

C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.5E-32//171aa//36%//P21573

10 C-MAMMA1001754//&amp;quot;Homo sapiens CGI-11 protein mRNA, complete cds.&amp;quot;//0//1837bp//98%//AF132945

C-MAMMA1001757

C-MAMMA1001764

C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45//351aa//38%//Q58556

15 C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991

C-MAMMA1001790

C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%//Q07230

C-MAMMA1001858

C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%//P22793

20 C-MAMMA1001970

C-MAMMA1002042

C-MAMMA1002068

C-MAMMA1002153

C-MAMMA1002156

25 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//157aa//70%//P15880

C-MAMMA1002174

C-MAMMA1002209

C-MAMMA1002219//&amp;quot;Homo sapiens mRNA for KIAA1067 protein, partial cds.&amp;quot;//1.1E-181//861bp//98%//AB028990

30 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//8.8E-217//310aa//86%//P70541

C-MAMMA1002243

C-MAMMA1002268//&amp;quot;Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.&amp;quot;//1E-190//1624bp//76%//AF068748

35 C-MAMMA1002269

C-MAMMA1002292

C-MAMMA1002294

C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.1E-214//881bp//97%//AJ011679

40 C-MAMMA1002312

C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991

C-MAMMA1002333

C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%//P40882

C-MAMMA1002353

45 C-MAMMA1002355

C-MAMMA1002356

C-MAMMA1002362

C-MAMMA1002380

C-MAMMA1002384

50 C-MAMMA1002427

C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623

C-MAMMA1002485//&amp;quot;Homo sapiens stanniocalcin-related protein mRNA, complete cds.&amp;quot;//0//1822bp//99%//AF098462

C-MAMMA1002524

C-MAMMA1002524//&amp;quot;Homo sapiens stanniocalcin-related protein mRNA, complete cds.&amp;quot;//0//1822bp//99%//AF098462

C-MAMMA1002530//&amp;quot;Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete

cds.&quot;:0//1910bp//99%/AF065214

C-MAMMA1002554

C-MAMMA1002585//&quot;Homo sapiens mRNA for KIAA0860 protein, complete cds.&quot;:0//1405bp//99%/AB020667

5 C-MAMMA1002598

C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)//9.5E-16//159aa//37%/Q09931

10 C-MAMMA1002655//&quot;Homo sapiens mRNA for ganglioside sialidase, complete cds.&quot;:0//1515bp//99%/AB008185

C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME)//1.1E-45//618aa//26%/P27550

C-MAMMA1002673

15 C-MAMMA1002684//&quot;Homo sapiens mRNA for KIAA0214 protein, complete cds.&quot;:0//3174bp//99%/D86987

C-MAMMA1002711

C-MAMMA1002769//&quot;Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.&quot;:2.2E-25//330bp//77%/AF011794

C-MAMMA1002775

20 C-MAMMA1002782

C-MAMMA1002796

C-MAMMA1002807

C-MAMMA1002838

25 C-MAMMA1002842//&quot;Mus musculus c-Cb1 associated protein CAP mRNA, complete cds.&quot;:2.6E-58//373bp//81%/U58883

C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN)//1.4E-160//305aa//85%/P48059

C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN)//5.7E-30//214aa//35%/P48060

30 C-MAMMA1002886

C-MAMMA1002890

C-MAMMA1002938//&quot;Homo sapiens mRNA for KIAA0698 protein, complete cds.&quot;:8.4E-252//1139bp//100%/AB014598

C-MAMMA1002964

35 C-MAMMA1003011//HESTONE MACRO-H2A.1//2.7E-123//370aa//66%/Q02874

C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7)//7.4E-46//332aa//36%/P06746

C-MAMMA1003015

C-MAMMA1003019

40 C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)//1.9E-13//108aa//33%/P23851

C-MAMMA1003039

C-MAMMA1003044

C-MAMMA1003049

C-MAMMA1003056

45 C-MAMMA1003057//MD6 PROTEIN//3.1E-225//419aa//97%/Q60584

C-MAMMA1003066

C-MAMMA1003099

C-MAMMA1003104

50 C-MAMMA1003113//&quot;Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.&quot;:1.1E-234//1178bp//86%/AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA)//2.2E-105//217aa//89%/P46735

C-MAMMA1003135

C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//4.3E-218//996bp//99%/Y15062

C-MAMMA1003150//&quot;Homo sapiens mRNA for KIAA1096 protein, partial cds.&quot;:0//1210bp//99%/U58883

C-MAMMA1003150//&quot;Homo sapiens mRNA for KIAA1096 protein, partial cds.&quot;:0//1210bp//99%/U58883

C-N12HM1000032

C-NT2RM1000035//&quot;Human mRNA for KIAA0199 gene, partial cds.&quot;//0//2948bp//99%//D83782  
 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-)  
 (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596  
 C-NT2RM1000055//&quot;Homo sapiens mRNA for KIAA0829 protein, partial cds.&quot;//0//3111bp//99%//  
 5 AB020636  
 C-NT2RM1000059  
 C-NT2RM1000062  
 C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 10 C-NT2RM1000119  
 C-NT2RM1000127  
 C-NT2RM1000131//&quot;Homo sapiens mRNA for KIAA0792 protein, complete cds.&quot;//0//2980bp//99%//  
 AB018335  
 C-NT2RM1000132//&quot;Homo sapiens NADH:ubiquinone oxidoreductas NDUFS6 subunit mRNA, nuclear gene  
 15 encoding mitochondrial protein, complete cds.&quot;//7.8E-110//516bp//99%//AF044959  
 C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-3 8//469aa//27%//P49902  
 C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-  
 CINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072  
 C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 20 SPAC10F6.02C.//1.1E-10//94aa//47%//O42643  
 C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//  
 AJ245820  
 C-NT2RM1000244//&quot;Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.&quot;//2E-126//592bp//  
 99%//U81002  
 25 C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%//X73882  
 C-NT2RM1000256//&quot;Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete  
 cds.&quot;//0//3012bp//99%//AB016789  
 C-NT2RM1000260//&quot;Human mRNA for KIAA0130 gene, complete cds.&quot;//0//3139bp//98%//D50920  
 C-NT2RM1000271  
 30 C-NT2RM1000300  
 C-NT2RM1000314//&quot;Human mRNA for KIAA0159 gene, complete cds.&quot;//0//4349bp//99%//D63880  
 C-NT2RM1000354//&quot;Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.  
 &quot;//7.4E-245//2101bp//68%//AF111423  
 C-NT2RM1000355//&quot;Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.&quot;//0//  
 35 1599bp//99%//AF152462  
 C-NT2RM1000365  
 C-NT2RM1000377//&quot;Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.&quot;/  
 //3.2E-196//1016bp//94%//AF179212  
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//  
 40 0.000000019//67aa//31%//P53915  
 C-NT2RM1000399  
 C-NT2RM1000430//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//  
 1.4E-185//1486bp//81%//AF084928  
 C-NT2RM1000555//&quot;Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//  
 45 AB020692  
 C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//  
 30%//Q08372  
 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636  
 C-NT2RM1000661//&quot;Homo sapiens translation initiation factor 4e mRNA, complete cds.&quot;//4.3E-210//  
 50 960bp//99%//AF038957  
 C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989  
 C-NT2RM1000672  
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440  
 C-NT2RM1000699  
 C-NT2RM1000742//&quot;Homo sapiens X-chromosome antigen mRNA, complete cds.&quot;//0//3524bp//99%//  
 AF027208

C-NT2RM1000746//&quot;Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.&quot;//6.70E-227//1043bp//99%//AF141310

C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202

C-NT2RM1000772//VEGETATTOLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808

C-NT2RM1000780

C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.1E-98//571bp//89%//Z97207

C-NT2RM1000802

C-NT2RM1000811//&quot;Homo sapiens AC133 antigen mRNA, complete cds.&quot;//0//3524bp//99%//AF027208

C-NT2RM1000826//&quot;Homo sapiens mRNA for KIAA0885 protein, complete cds.&quot;//0//2885bp//99%//AB020692

C-NT2RM1000829

C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%//P16157

C-NT2RM1000852//&quot;Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.&quot;//0//2206bp//99%//AF077033

C-NT2RM1000857//&quot;Homo sapiens mRNA for KIAA0962 protein, partial cds.&quot;//0//3716bp//99%//AB023179

C-NT2RM1000874//&quot;Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.&quot;//1.4E-244//1113bp//99%//AF043733

C-NT2RM1000882//&quot;Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.&quot;//4.30E-122//1394bp//69%//AF126799

C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa//30%//P34537

C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700

C-NT2RM1000898//&quot;ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR)&quot;//8.9E-26//229aa//29%//P02583

C-NT2RM1000905//&quot;Homo sapiens HSPC021 mRNA, complete cds.&quot;//0//1480bp//99%//AF077207

C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1E-15//266aa//26%//P46577

C-NT2RM1000927

C-NT2RM1000962

C-NT2RM1000978

C-NT2RM1001003//&quot;Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.&quot;//0//2230bp//99%//AF030233

C-NT2RM1001043

C-NT2RM1001066

C-NT2RM1001072//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148)&quot;//8.3E-47//259aa//35%//P08487

C-NT2RM1001085//&quot;Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.&quot;//3.7E-32//460bp//64%//AF053768

C-NT2RM1001102//&quot;Human HEM45 mRNA, complete cds.&quot;//2.3E-27//482bp//63%//U88964

C-NT2RM1001105

C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp//99%//AL049943

C-NT2RM2000420

C-NT2RM2000566//&quot;Homo sapiens integrin alpha-7 mRNA, complete cds.&quot;//0//2519bp//96%//AF032108

C-NT2RM2000609

C-NT2RM2000612//&quot;Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.&quot;//2.6E-106//1069bp//74%//U35776

C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6) //2.9E-103//249aa//73%//P28160

C-NT2RM2001588

C-NT2RM2001589//&quot;Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp//99%//AL049943

C-NT2RM2001590//&quot;Homo sapiens secb1 armolq mRNA, complete cds.&quot;//0//2601bp//99%//AF084456

C-NT2RM2001632//KES 1 PROTEIN//1.40E-31//342aa//34%//P35844

C-NT2RM2001648//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2421bp//99%//AF084458

5 C-NT2RM2001652//&quot;Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.&quot;//0//2608bp//99%//AF111162

C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN//3.4E-39//161aa//34%//P20107

C-NT2RM2001664//&quot;Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.&quot;//0//2471bp//99%//AF044195

10 C-NT2RM2001668//&quot;Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds.&quot;//6.2E-16//464bp//62%//AF083391

C-NT2RM2001671//&quot;Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.&quot;//0//1843bp//94%//U21155

C-NT2RM2001675

C-NT2RM2001681

15 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I//4.60E-20//253aa//30%//Q09674

C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA//0//2016bp//99%//AF103804

C-NT2RM2001696

20 C-NT2RM2001698//&quot;Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.&quot;//6.2E-253//1170bp//99%//AB028600

C-NT2RM2001700//&quot;ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VL-CAD) (FRAGMENT).&quot;//5.7E-130//536aa//49%//P50544

C-NT2RM2001716

C-NT2RM2001723

25 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)//7.2E-16//381aa//27%//Q09931

C-NT2RM2001743//&quot;Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.&quot;//0//1498bp//99%//AF011792

30 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210//8.8E-11//119aa//36%//Q92609

C-NT2RM2001760//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//0//2379bp//99%//AF084458

C-NT2RM2001768

C-NT2RM2001771//ZINC FINGER PROTEIN 135//6.4E-154//394aa//64%//P52742

35 C-NT2RM2001782//&quot;Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.&quot;//0//1470bp//99%//AF135422

C-NT2RM2001784

C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201)//0//2146bp//99%//AL050118

40 C-NT2RM2001813

C-NT2RM2001823//CHD1 PROTEIN//1.8E-106//631aa//39%//P32657

C-NT2RM2001839//&quot;Homo sapiens calumein (Calu) mRNA, complete cds.&quot;//0//2415bp//97%//AF013759

C-NT2RM2001840

45 C-NT2RM2001855

C-NT2RM2001867//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//967bp//99%//AB023160

C-NT2RM2001879

50 C-NT2RM2001983//&quot;Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.&quot;//0//1658bp//98%//AF089816

C-NT2RM2002145//&quot;Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.&quot;//8.5E-191//1524bp//81%//AF084928

C-NT2RM4000027

C-NT2RM4000030//LAS1 PROTEIN//5.6E-12//184aa//32%//P36146

C-NT2RM4000035

C-NT2RM4000035//&quot;Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201)//0//2146bp//99%//AL050118

C-NT2RM4000035//&quot;Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201)//0//2146bp//99%//AL050118

C-NT2RM4000156//H.sapiens HPBR11-7 gene//3.6E-21//785bp//60%//X67336

- C-NT2RM4000167//&quot;Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.&quot;//0//1946bp//99%//AF071592
- C-NT2RM4000199
- C-NT2RM4000200
- 5 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2)//4.9E-32//170aa//41%//Q16600
- C-NT2RM4000233//&quot;Mus musculus semaphorin VIa mRNA, complete cds.&quot;//3.4E-231//1395bp//86%//AF030430
- C-NT2RM4000244
- C-NT2RM4000251
- 10 C-NT2RM4000265
- C-NT2RM4000324
- C-NT2RM4000327
- C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292
- C-NT2RM4000425
- 15 C-NT2RM4000433//&quot;Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.&quot;//4.1E-271//2085bp//77%//AF062476
- C-NT2RM4000514
- C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29)//2.4E-89//389aa//43%//007230
- C-NT2RM4000532
- 20 C-NT2RM4000534
- C-NT2RM4000603
- C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808
- C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.7E-146//420aa//60%//P27550
- 25 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aa//30%//P74168
- C-NT2RM4000689
- C-NT2RM4000698
- C-NT2RM4000700
- C-NT2RM4000712//&quot;Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.&quot;//1E-136//1104bp//77%//AF022789
- 30 C-NT2RM4000717
- C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154
- C-NT2RM4000734//&quot;Homo sapiens mRNA for KIAA0760 protein, partial cds.&quot;//0//2273bp//99%//AB018303
- 35 C-NT2RM4000741//&quot;Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.&quot;//0//2184bp//99%//D88208
- C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53%//Q99676
- C-NT2RM4000764
- C-NT2RM4000778
- 40 C-NT2RM4000787
- C-NT2RM4000790
- C-NT2RM4000795//&quot;Homo sapiens mRNA for KIAA0951 protein, complete cds.&quot;//0//1847bp//96%//AB023168
- C-NT2RM4000796
- 45 C-NT2RM4000798//&quot;Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.&quot;//0//2603bp//99%//AF084521
- C-NT2RM4000813
- C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682
- 50 C-NT2RM4000833
- C-NT2RM4000848
- C-NT2RM4000852
- C-NT2RM4000855
- C-NT2RM4000887
- C-NT2RM4000895
- C-NT2RM4000945
- C-NT2RM4000975
- C-NT2RM4001002//Homo sapiens mRNA, cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2259bp//

100%//AL050092  
 C-NT2RM4001032  
 C-NT2RM4001047//M025 PROTEIN//8E-140//333aa//80%//Q06138  
 C-NT2RM4001054//&quot;Homo sapiens sec61 homolog mRNA, complete cds.&quot;//3.1E-190//1315bp//81%//  
 5 AF077032  
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I//0.000000032//  
 165aa//33%//Q09820  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II//5.9E-86//292aa//  
 48%//Q09417  
 10 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D//1E-11//103aa//38%//Q01704  
 C-NT2RM4001151  
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN//4.1E-197//445aa//78%//Q27969  
 C-NT2RM4001160  
 C-NT2RM4001187  
 15 C-NT2RM4001191//&quot;Homo sapiens clone 24963 mRNA sequence, complete cds.&quot;//0//1950bp//99%//  
 AF131737  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135//9.5E-135//375aa//60%//P52742  
 C-NT2RM4001203//&quot;Homo sapiens mRNA for KIAA0839 protein, partial cds.&quot;//0//3047bp//99%//  
 AB020646  
 20 C-NT2RM4001204//&quot;Homo sapiens mRNA for KIAA1089 protein, partial cds.&quot;//0//2349bp//99%//  
 AB029012  
 C-NT2RM4001217//&quot;Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds.&quot;//  
 7.3E-148//1409bp//72%//AF059611  
 C-NT2RM4001256//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//4.30E-55//  
 25 289bp//77%//AF129131  
 C-NT2RM4001258  
 C-NT2RM4001309  
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-  
 3-KINASE) (PI3K)//3.50E-35//124aa//65%//P54676  
 30 C-NT2RM4001316//&quot;ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.3) (MCAD).&quot;//2.3E-31//334aa//30%//P08503  
 C-NT2RM4001320//&quot;Homo sapiens mRNA for Neuroblastoma, complete cds.&quot;//1.8E-39//728bp//64%//  
 D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN)//1E-28//171aa//37%//P32626  
 35 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION//8.1E-  
 30//265aa//33%//P53742  
 C-NT2RM4001347//&quot;Homo sapiens NY-REN-25 antigen mRNA, partial cds.&quot;//0//2300bp//99%//  
 AF155103  
 C-NT2RM4001371//&quot;Homo sapiens IDN3 mRNA, partial cds.&quot;//0//2524bp//99%//AB019494  
 40 C-NT2RM4001382//&quot;Homo sapiens RanBP7/importin 7 mRNA, complete cds.&quot;//2.2E-237//1079bp//  
 99%//AF098799  
 C-NT2RM4001384  
 C-NT2RM4001410  
 C-NT2RM4001411//&quot;Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA,  
 45 complete cds.&quot;//0//1962bp//87%//AF020526  
 C-NT2RM4001412//&quot;Homo sapiens nGAP mRNA, complete cds.&quot;//0//1918bp//99%//AF047711  
 C-NT2RM4001414  
 C-NT2RM4001437  
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS)//  
 50 1.4E-118//444aa//46%//P73505  
 C-NT2RM4001454  
 C-NT2RM4001455  
 C-NT2RM4001483//ZINC FINGER PROTEIN 136//5.1E-106//357aa//55%//P52737  
 C-NT2RM4001489//&quot;Homo sapiens mRNA for KIAA0685 protein, complete cds.&quot;//0//3047bp//99%//  
 AB020646  
 C-NT2RM4001557//&quot;Homo sapiens mRNA for KIAA1040 protein, partial cds.&quot;//0//1547bp//97%//  
 AB028963

C-NT2RM4001565

C-NT2RM4001566//&quot;Homo sapiens mRNA for KIAA1114 protein, complete cds.&quot;://0//1900bp//99%//AB029037

C-NT2RM4001582//&quot;Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.&quot;//  
1.5E-284//1082bp//90%//AF071317

C-NT2RM4001592//&quot;Homo sapiens mRNA for KIAA1122 protein, partial cds.&quot;://0//2170bp//99%//  
AB032948

C-NT2RM4001594

C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750

C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%//Q12600

C-NT2RM4001629//&quot;MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).&quot;//1.5E-93//278aa//38%//Q13368

C-NT2RM4001650

C-NT2RM4001662

C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84//410aa//42%/P37339

C-NT2RM4001682

C-NT2RM4001710

C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q14141

C-NT2RM4001715

C-NT2RM4001731//&quot;Homo sapiens mRNA for KIAA1004 protein, partial cds.&quot;//0//1922bp//100%//  
AB023221

C-NT2RM4001746

C-NT2RM4001754

C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-)//4.1E-186//639aa//58%//Q05512

C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q03164

C-NT2RM4001810//&quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&quot;//0//2377bp//99%//  
AB020670

C-NT2RM4001813//LECTIN BRA-2//0.00000048//114aa//30%//P17346

C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)///2.9E-55//325aa//37%//P28160

C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//5.9E-161//481aa//56%//P51523

C-NT2RM4001836

C-NT2RM4001841//&quot;Homo sapiens mRNA for KIAA0920 protein, complete cds.&quot;//0//1861bp//98%//  
AB023137

C-NT2RM4001842

C-NT2RM4001856

C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%//P79779

C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//4.3E-244//1248bp//94%/Y17711

C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//6.5E-23//184aa//36%//Q15404

C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-)//5.9E-09//268aa//26%//P47486

C-NT2RM4001922//&quot;Homo-sapiens mRNA for KIAA0957 protein, complete cds.&quot;://0//2165bp//99%/AB023174

C-NT2RM4001930//&quot;Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.&quot;://0//1930bp//99%//AF102851

C-NT2RM4001940//&quot;Homo sapiens timeless homolog mRNA, complete cds.&quot;://0//2087bp//99%//AF098162

C-NT2RM4001953

C-NT2RM4001965

C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%//X99330

C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%//P51523

**AUTHORS:**

\* HM401181 & 1182 are the same as HM401179 & 1180.

DOI:10.1002/AIN.140j.&quot;#x2E173.2E-177281aa/30%#P16170

C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1

INTERGENIC REGION.//6.9E-94//589aa//35%/P42935

C-NT2RM4002018

C-NT2RM4002034//&quot;Homo sapiens hiwi mRNA, partial cds.&quot;//1.9E-53//1585bp//60%/AF104260

C-NT2RM4002044

5 C-NT2RM4002054

C-NT2RM4002063//&quot;Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.&quot;//0//1865bp//99%/U82267

C-NT2RM4002066//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.&quot;//1.50E-211//1123bp//71%/AF117755

10 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%/Q04652

C-NT2RM4002128

C-NT2RM4002140

C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%/P24014

C-NT2RM4002161//&quot;Homo sapiens laforin (EPM2A) mRNA, complete cds.&quot;//0//2671bp//99%/AF084535

15 C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%/P21590

C-NT2RM4002189//&quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&quot;//6.2E-33//688aa//27%/P08640

C-NT2RM4002205//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//3E-37//122aa//72%/Q07803

20 C-NT2RM4002213//&quot;Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.&quot;//0//2452bp//100%/AF157028

C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%/P40809

C-NT2RM4002251//&quot;ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYL-TRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-TI).&quot;//2.2E-36//320aa//38%/P27808

C-NT2RM4002256

C-NT2RM4002266

C-NT2RM4002281

30 C-NT2RM4002287

C-NT2RM4002294

C-NT2RM4002301

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33 %/P48778

C-NT2RM4002339

35 C-NT2RM4002344

C-NT2RM4002373//&quot;Homo sapiens mRNA for KIAA0649 protein, complete cds.&quot;//0//2666bp//99%/AB014549

C-NT2RM4002374

C-NT2RM4002383

40 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//1.3E-29//275aa//30%/P27095

C-NT2RM4002438//&quot;Xenopus laevis putative Zic3 binding protein mRNA, complete cds.&quot;//1.1E-49//611bp//70%/AF129131

C-NT2RM4002446

45 C-NT2RM4002452

C-NT2RM4002457

C-NT2RM4002460//&quot;ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].&quot;//0.0000016//226aa//24%/P51515

C-NT2RM4002493

50 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%/Q00808

C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%/P55137

C-NT2RM4002558//&quot;Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.&quot;//0//1797bp//99%/AF055899

C-NT2RM4002567

C-NT2RM4002568

C-NT2RM4002594//MSH-1.//1.1E-15//1000aa//27%/U00000

C-NT2RM4002623//ASPARTYL- tRNA SYNTHETASE (EC 6.1.1.2) (ASPARTATE--tRNA LIGASE) (ASPRS).//2.3E-101//488aa//45%/U032038

- C-NT2RP1000324  
C-NT2RP1000363//&quot;Homo sapiens mRNA for KIAA0638 protein, partial cds.&quot;//0//1345bp//99%  
AB014538  
C-NT2RP1000418  
5 C-NT2RP1000513//&quot;Human NifU-like protein (hNifU) mRNA, partial cds.&quot;//6.50E-171//516bp//99%  
U47101  
C-NT2RP1000721  
C-NT2RP1000730  
C-NT2RP1000767  
10 C-NT2RP1000836  
C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//  
33%//Q09531  
C-NT2RP1000943  
C-NT2RP1001033//&quot;Homo sapiens delta-tubulin mRNA, complete cds.&quot;//2.10E-285//1290bp//100%  
15 AF201333  
C-NT2RP1001073//&quot;Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.  
&quot;//8.1E-107//504bp//99%//AF182291  
C-NT2RP1001199  
C-NT2RP1001248  
20 C-NT2RP1001253//&quot;Homo sapiens oscillin (hLn) mRNA, complete cds.&quot;//0//2020bp//99%//AF029914  
C-NT2RP1001286  
C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1 //1.80E-38//258aa//32%//Q12024  
C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1 //1.80E-38//258aa//32%//Q12024  
C-NT2RP1001310//&quot;Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear  
25 gene for mitochondrial product.&quot;//0//1732bp//99%//AF176006  
C-NT2RP1001361//&quot;Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA,  
complete cds.&quot;//6.5E-116//541bp//100%//AF070652  
C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.7E-22//  
284aa//25%//P40074  
30 C-NT2RP1001432  
C-NT2RP2000040//&quot;Homo sapiens mRNA for KIAA0747 protein, partial cds.&quot;//0//2648bp//99%  
AB013290  
C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.9E-20//265bp//73%  
AJ242730  
35 C-NT2RP2000098  
C-NT2RP2000108  
C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W//9.7E-41//278aa//36%//P40556  
C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD  
SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//  
40 7.1E-12//213aa//23%//P35251  
C-NT2RP2000289  
C-NT2RP2000327  
C-NT2RP2000337  
C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910  
45 C-NT2RP2000459  
C-NT2RP2000498  
C-NT2RP2000758  
C-NT2RP2001137  
C-NT2RP2001149  
50 C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%//P37370  
C-NT2RP2001173//&quot;Homo sapiens mRNA for KIAA0480 protein, complete cds.&quot;//0//1780bp//99%  
AB007949  
C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6E-10//88aa//38%  
P18722  
C-NT2RP2001211  
C-NT2RP2001268//&quot;Homo sapiens mRNA for KIAA0610 protein, partial cds.&quot;//0//3301bp//98%  
AB018353

- C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.4E-91//179aa//99%/P28663  
 C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%/P20107  
 C-NT2RP2001312  
 5 C-NT2RP2001327//"TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)."//5.5E-116//311aa//71%/Q13829  
 C-NT2RP2001328  
 C-NT2RP2001366  
 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//2E-11//403aa//25%/Q02817  
 10 C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.4E-192//581aa//54%/P93647  
 C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%/Y18004  
 C-NT2RP2001420//"Mus musculus nuclear protein NIP45 mRNA, complete cds."//9E-112//742bp//82%/U76759  
 15 C-NT2RP2001450  
 C-NT2RP2001467  
 C-NT2RP2001506  
 C-NT2RP2001511//"Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//3.2E-297//2206bp//75 %/AF093097  
 20 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%/Y14494  
 C-NT2RP2001536//"Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds."//0//2326bp//99%/AF035586  
 C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%/Q60992  
 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME 1.//8.2E-29//294aa//31%/Q09837  
 25 C-NT2RP2001581  
 C-NT2RP2001597//"RYANODINE RECEPTOR, CARDIAC MUSCLE."//0.000000036//127aa//36%/P30957  
 C-NT2RP2001628  
 30 C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%/P42897  
 C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-PHOSPHATE SYNTHETASE) (DIMETHYLLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANS-FERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//97%/P14324  
 35 C-NT2RP2001813  
 C-NT2RP2001883//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//2306bp//99%/AF132936  
 C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%/P53946  
 C-NT2RP2001947  
 40 C-NT2RP2001985//"Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds."//2.00E-38//435bp//67%/AF090989  
 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%/Q08469  
 C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.7E-47//247aa//52%/P35331  
 45 C-NT2RP2002058//"Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds."//0//2510bp//99%/AF083217  
 C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.7//1.5E-294//1334bp//99%/AF052183  
 C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%/P18490  
 50 C-NT2RP2002079//"HISTONE H1, GONADAL."//4.4E-11//214aa//34%/P02256  
 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%/AJ007509  
 C-NT2RP2002185//"Homo sapiens ubiquitin mRNA, complete cds."//0//1789bp//99%/AF176069  
 C-NT2RP2002193//"Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds."//0//2809bp//99%/AB021868  
 C-NT2RP2002223  
 C-NT2RP2002252//"Mus musculus (clone pV2mSin3A9) mSin3A9 mRNA, complete cds."//0//3118bp//91%/L38621

C-NT2RP2002292  
 C-NT2RP2002408  
 C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%/P46037  
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1 //6.50E-07//171aa//27%/P30620  
 5 C-NT2RP2002498  
 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-14//537aa//49%/Q02386  
 C-NT2RP2002520//"Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds."//3.70E-34//668bp//61%/AF105427  
 C-NT2RP2002549  
 10 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%/P19076  
 C-NT2RP2002706  
 C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%/P55194  
 C-NT2RP2002800  
 15 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%/P14922  
 C-NT2RP2002891  
 C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.1E-87//395aa//40%/Q18964  
 C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%/P52737  
 20 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%/P70700  
 C-NT2RP2003034  
 C-NT2RP2003099  
 C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%/P13117  
 25 C-NT2RP2003157//"Homo sapiens CGI-74 protein mRNA, complete cds."//0//2037bp//99%/AF151832  
 C-NT2RP2003158//"Homo sapiens mRNA for proteasome subunit p58, complete cds."//0//2091bp//99%/D67025  
 C-NT2RP2003165  
 30 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%/AJ242978  
 C-NT2RP2003277//"Homo sapiens mRNA for KIAA0625 protein, partial cds."//0//3788bp//99%/AB014525  
 C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%/Q23400  
 35 C-NT2RP2003297  
 C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%/Q07866  
 C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%/P17886  
 C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%/P48754  
 40 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%/AJ133769  
 C-NT2RP2003393  
 C-NT2RP2003445  
 C-NT2RP2003466//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds."//7//2194bp//99%/AF126799  
 45 C-NT2RP2003480//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//3012bp//99%/AF125158  
 C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4E-14//106aa//46%/P04175  
 50 C-NT2RP2003511  
 C-NT2RP2003513//"Human mRNA for KIAA0270 gene, partial cds."//0//2137bp//97%/D87460  
 C-NT2RP2003567//"Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//2343bp//99%/AB007931  
 C-NT2RP2003604//"Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds."//0//1101bp//99%/AF126799  
 C-NT2RP2003694  
 C-NT2RP2003713//"Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds."//0//2018bp//99%/AF073344

- C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%//P53620
- C-NT2RP2003764
- C-NT2RP2003769
- 5 C-NT2RP2003777
- C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.7E-21//137aa//43%//Q11076
- C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.00000016//117aa//29%//Q91955
- 10 C-NT2RP2003981//&quot;Homo sapiens mRNA for KIAA0804 protein, partial cds.&quot;//0//3046bp//99%//AB018347
- C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026).//0//2514bp//99%//AL050367
- C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599
- 15 C-NT2RP2004066//&quot;Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33, complete sequence.&quot;//0//2410bp//99%//AL034555
- C-NT2RP2004081
- C-NT2RP2004124
- C-NT2RP2004152
- 20 C-NT2RP2004165
- C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//5.6E-31//424aa//28%//007231
- C-NT2RP2004239//&quot;Homo sapiens lok mRNA for protein kinase, complete cds.&quot;//0//3044bp//99%//AB015718
- 25 C-NT2RP2004245
- C-NT2RP2004364
- C-NT2RP2004365
- C-NT2RP2004366//&quot;Homo sapiens mRNA for KIAA0986 protein, partial cds.&quot;//0//2790bp//97%//AB023203
- 30 C-NT2RP2004373
- C-NT2RP2004476//&quot;Homo sapiens cyclin L ania-6a mRNA, complete cds.&quot;//0//2075bp//99%//AF180920
- C-NT2RP2004551
- C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//625aa//40%//Q09903
- 35 C-NT2RP2004600
- C-NT2RP2004664//&quot;Homo sapiens mRNA for KIAA0460 protein, partial cds.&quot;//0//2368bp//99%//AB007929
- C-NT2RP2004743
- C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.3E-26//190aa//41-%//P38692
- 40 C-NT2RP2004816//&quot;Homo sapiens H beta 58 homolog mRNA, complete cds.&quot;//0//2144bp//96%//AF054179
- C-NT2RP2004861
- C-NT2RP2004897
- 45 C-NT2RP2004933//&quot;Homo sapiens mRNA for ZIP-kinase, complete cds.&quot;//0//2103bp//99%//AB007144
- C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386
- C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4E-91//218aa//44%//Q92089
- 50 C-NT2RP2005162//&quot;Homo sapiens aspartyl aminopeptidase mRNA, complete cds.&quot;//0//1615bp//99%//AF005050
- C-NT2RP2005204//&quot;Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.&quot;//0//1262bp//99%//AF090385
- C-NT2RP2005227
- C-NT2RP2005288//&quot;Homo sapiens mRNA for KIAA0621 protein, partial cds.&quot;//0//1420bp//99%//AF066215
- C-NT2RP2005490//&quot;Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.&quot;//1.8E-175//1102bp//

83%//AF053628

C-NT2RP2005539//&amp;quot;Homo sapiens mRNA for KIAA0850 protein, complete cds.&amp;quot;//0//1560bp//99%//AB020657

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053

C-NT2RP2005722//&amp;quot;Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.&amp;quot;//0//2545bp//99%//AB011414

C-NT2RP2005732

C-NT2RP2005784//&amp;quot;Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.&amp;quot;//0//2191bp//92%//AF155120

C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//318aa//31%//P40004

C-NT2RP2005859//&amp;quot;Homo sapiens mRNA for KIAA0863 protein, complete cds.&amp;quot;//0//1649bp//99%//AB020670

C-NT2RP2006023

C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//AL080155

C-NT2RP2006441

C-NT2RP3000002

C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//53%//Q05481

C-NT2RP3000055

C-NT2RP3000068

C-NT2RP3000080

C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.9E-123//436aa//50%//P46401

C-NT2RP3000092

C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692

C-NT2RP3000134

C-NT2RP3000149

C-NT2RP3000197

C-NT2RP3000207//&amp;quot;GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).&amp;quot;//2.9E-11//721aa//23%//P08640

C-NT2RP3000233//&amp;quot;Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins. Contains ESTs and GSSs, complete sequence.&amp;quot;//0//1462bp//99%//AL035424

C-NT2RP3000235

C-NT2RP3000247

C-NT2RP3000267

C-NT2RP3000299//&amp;quot;Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.&amp;quot;//0//2730bp//82%//D29766

C-NT2RP3000324

C-NT2RP3000341//&amp;quot;Homo sapiens mitochondrial inner membrane preprotein translocase Timl7a mRNA, nuclear gene encoding mitochondrial protein, complete cds.&amp;quot;//1.5E-246//1124bp//99%//AF106622

C-NT2RP3000393//&amp;quot;Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.&amp;quot;//5.8E-266//1373bp//86%//AF061817

C-NT2RP3000441//&amp;quot;Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.&amp;quot;//3.40E-42//645bp//67%//AF098066

C-NT2RP3000449

C-NT2RP3000451

C-NT2RP3000456

C-NT2RP3000542

C-NT2RP3000561

C-NT2RP3000566

C-NT2RP3000566

C-NT2RP3000578//HES1 PROTEIN.//3E-22//229aa//27%//P35843

C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

- C-NT2RP3000592  
 C-NT2RP3000622  
 C-NT2RP3000624  
 C-NT2RP3000685
- 5 C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140//1.2E-166//305aa//99%/014153  
 C-NT2RP3000742//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA  
 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)&quot;//4.1E-165//  
 371aa//49%/P10895  
 C-NT2RP3000753
- 10 C-NT2RP3000826  
 C-NT2RP3000865  
 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK)//7.7E-87//175aa//98%/Q03426  
 C-NT2RP3001007  
 C-NT2RP3001055
- 15 C-NT2RP3001111//&quot;Homo sapiens TRF-proximal protein mRNA, complete cds.&quot;//1.50E-149//731bp//  
 97%/AF097725  
 C-NT2RP3001120//ZINC FINGER PROTEIN 136//7.8E-170//512aa//58%/P52737  
 C-NT2RP3001126  
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO//0.00000031//207aa//29%/P52154
- 20 C-NT2RP3001232  
 C-NT2RP3001268//&quot;Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.&quot;//0//  
 3606bp//99%/AF198358  
 C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein//  
 1.3E-99//669bp//83%/Y18101
- 25 C-NT2RP3001274//&quot;Homo sapiens mRNA for KIAA1037 protein, partial cds.&quot;//0//2254bp//99%/  
 AB028960  
 C-NT2RP3001281  
 C-NT2RP3001297  
 C-NT2RP3001318
- 30 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT)//2.4E-16//175aa//28%/P51508  
 C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-  
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN)//3.6E-25//129aa//34%/P32089  
 C-NT2RP3001374  
 C-NT2RP3001428//NUCLEOPROTEIN TPR//1.4E-128//152aa//99%/P12270
- 35 C-NT2RP3001432  
 C-NT2RP3001447  
 C-NT2RP3001449//&quot;Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the  
 alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A,  
 -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA,  
 40 Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal  
 Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)  
 bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G  
 protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs,  
 complete sequence.&quot;//0//1827bp//99%/AL031282
- 45 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFI-  
 ER 2)//3.2E-90//157aa//59%/P36371  
 C-NT2RP3001459  
 C-NT2RP3001527//&quot;Human Spl40 protein (Spl40) mRNA, complete cds.&quot;//4.3E-290//793bp//93%/U63420
- 50 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T2.8D9.3 IN CHROMOSOME II//9.10E-10//158aa//  
 31%/Q10022  
 C-NT2RP3001580//&quot;Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.&quot;//  
 0//1730bp//85%/AF163665  
 C-NT2RP3001587//&quot;Human anthracycline-associated resistance ARX mRNA, complete cds.&quot;//0//1000bp//99%/U63420  
 C-NT2RP3001589  
 C-NT2RP3001601  
 C-NT2RP3001608

C-NT2RP3001671//&quot;Homo sapiens mRNA for KIAA0850 protein, complete cds.&quot;//0//2310bp//99%//  
 AB020657  
 C-NT2RP3001672//&quot;Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete  
 cds.&quot;//0//2836bp//99%//AF149046  
 5 C-NT2RP3001678  
 C-NT2RP3001688//&quot;Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA,  
 complete cds.&quot;//0//1695bp//99%//AF099013  
 C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.00000024//481aa//21%//  
 P25386  
 10 C-NT2RP3001698  
 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR//3.4E-33//161aa//32%//P54356  
 C-NT2RP3001716  
 C-NT2RP3001752  
 C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M)//1.8E-117//462aa//  
 15 55%//P52272  
 C-NT2RP3001844  
 C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013)//0//1528bp//  
 99%//AL050011  
 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1)//8.1E-125//302aa//  
 20 60%//P55347  
 C-NT2RP3001898//&quot;Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-  
 1,4-N-acetylglucosaminyltransferase IV, complete cds.&quot;//0//1587bp//100%//AB000624  
 C-NT2HP3001931  
 C-NT2RP3001969//TRICHOHYALIN//2.7E-11//442aa//23%//P37709  
 25 C-NT2RP3002002  
 C-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.50E-19211475bp//94%//X86779  
 C-NT2RP3002007//SAP1 PROTEIN//1.1E-68//474aa//32%//P39955  
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III//5.30E-25//139aa//  
 48%//Q09232  
 30 C-NT2RP3002045//&quot;Homo sapiens mRNA for KIAA0899 protein, partial cds.&quot;//0//33 85bp//99%//  
 AB020706  
 C-NT2RP3002056//&quot;Homo sapiens Rb binding protein homolog mRNA, partial cds.&quot;//0//2374bp//99%//  
 AF083249  
 C-NT2RP3002062//&quot;Homo sapiens mRNA for KIAA0873 protein, partial cds.&quot;//0//3764bp//99%//  
 35 AB020680  
 C-NT2RP3002081//&quot;Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.  
 &quot;//4.1E-233//1896bp//69%//AF111423  
 C-NT2RP3002097  
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN)//7.90E-09//181aa//22%//Q12387  
 40 C-NT2RP3002142  
 C-NT2RP3002146  
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN  
 GST1-HS)//2.8E-253//474aa//93%//P15170  
 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP7//1.9E-151//223aa//91%//Q02614  
 45 C-NT2RP3002166  
 C-NT2RP3002181  
 C-NT2RP3002244  
 C-NT2RP3002248  
 C-NT2RP3002273//SCD6 PROTEIN//1.30E-09//295aa//28%//P45978  
 50 C-NT2RP3002276  
 C-NT2RP3002304  
 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE)//  
 3.70E-43//318aa//37%//P05792  
 C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting //0//2276bp//99%//A1133421  
 C-NT2RP3002566  
 C-NT2RP3002588  
 C-NT2RP3002599  
 C-NT2RP3002631

- C-NT2RP3002650//&quot;Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.&quot;//0//2109bp//87%//AF165163
- C-NT2RP3002663//&quot;Homo sapiens putative glycolipid transfer protein mRNA, complete cds.&quot;//8.10E-263//1243bp//97%//AF103731
- 5 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2)//2.50E-73//179aa//36%//P13060
- C-NT2RP3002763
- C-NT2RP3002861
- C-NT2RP3002911
- C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN)//2E-111//551aa//42%//Q04652
- 10 C-NT2RP3002953//&quot;Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.&quot;//0//2388bp//99%//AF152498
- C-NT2RP3002988//&quot;Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds.&quot;//1.8E-292//1325bp//99%//AF080158
- C-NT2RP3003008
- 15 C-NT2RP3003101//&quot;Mouse mRNA for tetracycline transporter-like protein, complete cds.&quot;//3.6E-83//807bp//72%//D88315
- C-NT2RP3003204
- C-NT2RP3003278
- C-NT2RP3003282//&quot;Homo sapiens dynamin (DNM) mRNA, complete cds.&quot;//0//2596bp//98%//L36983
- 20 C-NT2RP3003290//&quot;Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.&quot;//1.5E-310//1468bp//82%//AB033922
- C-NT2RP3003302
- C-NT2RP3003313//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.&quot;//0//2476bp//99%//AF117657
- 25 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052)//1.3E-35//178aa//44%//Q62191
- C-NT2RP3003344
- C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084
- 30 C-NT2RP3003377
- C-NT2RP3003385//&quot;Mus musculus SKD3 mRNA, complete cds.&quot;//0//2133bp//85%//U09874
- C-NT2RP3003433
- C-NT2RP3003490//&quot;Homo sapiens mRNA for KIAA0725 protein, partial cds.&quot;//0//2437bp//99%//AB018268
- 35 C-NT2RP3003491//&quot;Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.&quot;//5.6E-36//842bp//62%//AF091624
- C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%//P17886
- C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820
- 40 C-NT2RP3004209//&quot;Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.&quot;//0//2320bp//99%//AF126736
- C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%//P52734
- C-NT2RP3004246
- 45 C-NT2RP3004258//&quot;Homo sapiens ZIS1 mRNA, complete cds.&quot;//0//1861bp//99%//AF065391
- C-NT2RP3004262//&quot;Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.&quot;//2.4E-248//1126bp//100%//AF088982
- C-NT2RP3004341
- C-NT2RP3004378
- 50 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1E-66//364bp//93%//AJ007798
- C-NT2RP3004428
- C-NT2RP3004451
- C-NT2RP3004454//&quot;Homo sapiens mRNA for KIAA0448 protein, complete cds.&quot;//0//2875bp//99%//AB007917
- C-NT2RP3004498//&quot;Mus musculus mRNA for C/EBP-beta, partial cds.&quot;//0//1777bp//80%//U83176
- C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.9E-295//893bp//92%//Y08260

- C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1)//3.7E-37//190aa//39%//P40484  
 C-NT2RP3004534//&quot;Mouse oncogene (ect2) mRNA, complete cds.&quot;//0//2075bp//87%//L11316  
 C-NT2RP4000528//NPL4 PROTEIN//9.8E-86//515aa//37%//P33755  
 5 C-NT2RP4000907//&quot;Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.&quot;//0//2127bp//86%//D45913  
 C-NT2RP4001029//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;//0//1711bp//90%//U20086  
 C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN//0.000016//186aa//29%//O24076  
 10 C-NT2RP4001389//KES1 PROTEIN//1.70E-31//342aa//34%//P35844  
 C-NT2RP4001442  
 C-NT2RP4001529//&quot;Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.&quot;//1.70E-255//1148bp//90%//U20086  
 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN)//1.10E-45//310aa//27%//P12868  
 15 C-OVARC1000106//&quot;TROPOMYOSIN 1, FUSION PROTEIN 33.&quot;//0.000032//165aa//27%//P49455  
 C-OVARC1000198  
 C-OVARC1000682//&quot;PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).&quot;//1.1E-209//293aa//95%//P39098  
 20 C-OVARC1000703  
 C-OVARC1000722//&quot;Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.&quot;//0//759bp//98%//AF038661  
 C-OVARC1000730  
 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN//0.000000017//78aa//48%//P25159  
 25 C-OVARC1000781  
 C-OVARC1000787  
 C-OVARC10008347/Homo sapiens mRNA for atopy related autoantigen CALCJ//2.8E-258//1183bp//99%//Y17711  
 C-OVARC1000846//NUCLEOLIN (PROTEIN C23)//0.0000097//109aa//30%//P08199  
 C-OVARC1000850//&quot;Homo sapiens PB39 mRNA, complete cds.&quot;//0//2095bp//99%//AF045584  
 30 C-OVARC1000862//M.musculus mRNA for FT1 //5.9E-226//1498bp//81%//Z67963  
 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1)//2.2E-50//206aa//52%//P40484  
 C-OVARC1000883  
 C-OVARC1000886  
 C-OVARC1000912  
 35 C-OVARC1000915//&quot;Homo sapiens histone deacetylase 5 mRNA, complete cds.&quot;//1.60E-121//591bp//97%//AF132608  
 C-OVARC1000924  
 C-OVARC1000964  
 C-OVARC1000984  
 40 C-OVARC1001004  
 C-OVARC1001010  
 C-OVARC1001011  
 C-OVARC1001032  
 C-OVARC1001044  
 45 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR//1.9E-35//76aa//98%//P43490  
 C-OVARC1001068//&quot;Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.&quot;//0//1819bp//99%//AF082657  
 C-OVARC1001074  
 C-OVARC1001092//&quot;Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).&quot;//2E-214//769bp//97%//AJ005897  
 50 C-OVARC1001107//&quot;Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.&quot;//6.1E-276//594bp//98%//AF167572  
 C-OVARC1001154//&quot;Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.&quot;//0.3E-665//1000bp//99%//AF038661  
 C-OVARC1001167  
 C-OVARC1001170

C-OVARC1001171//&quot;Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.&quot;  
//5.7E-151//436bp//92%//U94855

C-OVARC1001173

C-OVARC1001176

5 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510

C-OVARC1001188

C-OVARC1001232//&quot;CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT  
(CPSF 100 KD SUBUNIT).&quot;//5.10E-22//83aa//37%//Q10568

C-OVARC1001270

10 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//  
0.0000014//224aa//26%//P25976

C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444

C-OVARC1001344

C-OVARC1001369

15 C-OVARC1001372//&quot;Homo sapiens mRNA for KIAA0897 protein, partial cds.&quot;//0//840bp//97%//  
AB020704

C-OVARC1001391

C-OVARC1001399

20 C-OVARC1001417//&quot;Homo sapiens thyroid hormone receptor-associated protein complex component  
TRAP170 mRNA, complete cds.&quot;//0//1715bp//99%//AF135802

C-OVARC1001419//&quot;Homo sapiens GOK (STIM1) mRNA, complete cds.&quot;//4.9E-48//586bp//69%//  
U52426

C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111

C-OVARC1001453

25 C-OVARC1001476//&quot;Mus musculus YGR163w mRNA homologue, complete cds.&quot;//1.80E-187//  
510bp//89%//AB017616

C-OVARC1001480

C-OVARC1001489

30 C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE  
PROTEIN 1).//0//777aa//91%//P98161

C-OVARC1001525

C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081

C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//  
AF031165

35 C-OVARC1001600

C-OVARC1001610//&quot;Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete  
cds.&quot;//0//1870bp//99%//AF068302

C-OVARC1001702

40 C-OVARC1001703//&quot;Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.&quot;//3.5E-  
16//399bp//61%//AF133670

C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//  
38%//Q62267

C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-  
AZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106

45 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%//Q13796

C-OVARC1001731//&quot;TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.&quot;//4E-122//  
282aa//85%//P08942

C-OVARC1001745

50 C-OVARC1001762//&quot;N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-  
AMINO, ACETYLTRANSFERASE 1).&quot;//6.4E-85//514aa//34%//P12945

C-OVARC1001766//&quot;Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete  
cds.&quot;//0//963bp//99%//U97670

C-OVARC1001767//&quot;Homo sapiens mRNA for KIAA0675 protein, complete cds.&quot;//0//2083bp//99%//  
AB014575

C-OVARC1001795

C-OVARC1001802

C-OVARC1001809//&quot;Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.&quot;//2.7E-190//1624bp//76%//AF068748

C-OVARC1001828

C-OVARC1001846

5 C-OVARC1001861

C-OVARC1001879

C-OVARC1001880

C-OVARC1001883

C-OVARC1001916

10 C-OVARC1001928

C-OVARC1001942//&quot;N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1).&quot;//3.1E-81//497aa//35%//P12945

C-OVARC1001943//&quot;Mus musculus DEBT-91 mRNA, complete cds.&quot;//0//2035bp//87%//AF143859

C-OVARC1001950

15 C-OVARC1001987//&quot;Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.&quot;//2.3E-220//652bp//84%//AF061817

C-OVARC1002050//&quot;Homo sapiens mRNA for actin binding protein ABP620, complete cds.&quot;//0//1019bp//99%//AB029290

C-OVARC1002082

20 C-OVARC1002107

C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//035913

C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955

25 C-OVARC1002156

C-OVARC1002158

C-PLACE1000004//&quot;Homo sapiens IDN3-B mRNA, complete cds.&quot;//0//2365bp//99%//AB019602

C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643

C-PLACE1000048

30 C-PLACE1000050

C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154

C-PLACE1000081//&quot;Human SEC7 homolog Tic (TIC) mRNA, complete cds.&quot;//0//2077bp//99%//U63127

C-PLACE1000094

35 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8E-62//158aa//81%//P20290

C-PLACE1000214

C-PLACE1000236

C-PLACE1000246

40 C-PLACE1000292

C-PLACE1000308

C-PLACE1000332

C-PLACE1000453

45 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522

C-PLACE1000599

C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918

C-PLACE1000653//&quot;Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.&quot;//0//1992bp//99%//AF180371

50 C-PLACE1000656//&quot;Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).&quot;//2.1E-277//1260bp//99%//AJ005896

C-PLACE1000706//&quot;Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.&quot;//0//1366bp//99%//AF119043

C-PLACE1000712

C-PLACE1000786

AF132952

C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-

CIOGENITAL DYSPLASIA PROTEIN HOMOLOG)/7.10E-09//59aa//47%/P52734

C-PLACE1000849

C-PLACE1000856//&quot;Homo sapiens mRNA for KIAA0974 protein, partial cds.&quot;//0//1310bp//100%/AB023191

5 C-PLACE1000931

C-PLACE1000987//&quot;Homo sapiens mRNA for KIAA0724 protein, complete cds.&quot;//0//1749bp//99%/AB018267

C-PLACE1001010

C-PLACE1001015

10 C-PLACE1001024

C-PLACE1001062//&quot;Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence.&quot;//2.7E-32//470bp//71%/AC006020

C-PLACE1001104

C-PLACE1001168

15 C-PLACE1001171//MYOTUBULARIN./7.1E-84//198aa//73%/Q13496

C-PLACE1001185//&quot;Homo sapiens mRNA for KIAA0943 protein, partial cds.&quot;//0//1668bp//99%/AB023160

C-PLACE1001238//&quot;Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.&quot;//2E-202//1333bp//80%/D14336

20 C-PLACE1001280

C-PLACE1001294//M.musculus GEG-154 mRNA./4.3E-221//1057bp//78%/X71642

C-PLACE1001304//&quot;Homo sapiens zinc finger protein dp mRNA, complete cds.&quot;//0//2421bp//99%/AF153201

C-PLACE1001311

25 C-PLACE1001323

C-PLACE1001351

C-PLACE1001414

C-PLACE1001440

C-PLACE1001456

30 C-PLACE1001517//&quot;Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.&quot;//4.60E-112//392bp//87%/AB002137

C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1)/5.7E-130//244aa//99%/Q60809

C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)/1.4E-118//429aa//48%/P51523

35 C-PLACE1001634

C-PLACE1001640

C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-)/4.3E-66//174aa//45%/P91408

C-PLACE1001705

C-PLACE1001716

40 C-PLACE1001720

C-PLACE1001745

C-PLACE1001748//&quot;Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.&quot;//0//2602bp//99%/AF061243

C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein

45 TRP6//0//2900bp//99%/AJ006276

C-PLACE1001799

C-PLACE1001845//&quot;Mus musculus cyclin ania-6a mRNA, complete cds.&quot;//3.30E-31//925bp//62%/AF159159

C-PLACE1001897

50 C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72)/6.5E-58//112aa//100%/076094

C-PLACE1002157

C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYPE2)/0.00005//179aa//23%/P32591

C-PLACE1002251

C-PLACE1002319

C-PLACE1002395//&quot;Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.&quot;//7.9E-

100//966bp//75%//AB030505

C-PLACE1002477

C-PLACE1002493//&quot;Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.&quot;//1.7E-113//545bp//98%//AF042273

5 C-PLACE1002500

C-PLACE1002514

C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.2E-152//289aa//96%//P70396

C-PLACE1002537

C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%//P45890

10 C-PLACE1002583//&quot;GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).&quot;//5.6E-34//76aa//98%//P39087

C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%//P45340

C-PLACE1002625

15 C-PLACE1002655//ADSEVERIN (SCINDERIN)(SC).//2.5E-278//543aa//92%//Q28046

C-PLACE1002768

C-PLACE1002782//&quot;Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.&quot;//3.8E-43//385bp//77%//U50927

C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973

20 C-PLACE1002853

C-PLACE1002908//&quot;Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.&quot;//0//1654bp//99%//AB028600

C-PLACE1002962

C-PLACE1002968

25 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091

C-PLACE1003025

C-PLACE1003027//&quot;Homo sapiens mRNA for KIAA0516 protein, partial cds.&quot;//2.1E-314//1417bp//100%//AB011088

C-PLACE1003044//&quot;Homo sapiens mRNA for KIAA0829 protein, partial cds.&quot;//0//1382bp//96%//AB020636

30 C-PLACE1003176

C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%//Q15391

C-PLACE1003256

35 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa//47%//P21541

C-PLACE1003343

C-PLACE1003361

C-PLACE1003366//&quot;Homo sapiens otoferin (OTOF) mRNA, complete cds.&quot;//1.4E-78//542bp//67%//AF107403

40 C-PLACE1003373

C-PLACE1003375

C-PLACE1003394//&quot;Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.&quot;//2.30E-150//774bp//94%//M83680

C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.3E-40//278aa//36%//P40556

45 C-PLACE1003454

C-PLACE1003478

C-PLACE1003516

C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136

C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//Q09475

50 C-PLACE1003528

C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//7.7E-68//404aa//33%//P32802

C-PLACE1003584

C-PLACE1003590

C-PLACE1003605//HAP5 TRANSCRIPTIONAL

ACTIVATOR.//0.00000023//82aa//35%//Q02516

C-PLACE1003618

C-PLACE1003638

C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%//P52742

5 C-PLACE1003760//&quot;Homo sapiens tetraspanin TM4-A mRNA, complete cds.&quot;//5.2E-289//1313bp//97%//AF133423

C-PLACE1003768

C-PLACE1003795

C-PLACE1003886

10 C-PLACE1003888//&quot;Homo sapiens mRNA for KIAA1092 protein, partial cds.&quot;//0//2057bp//99%//AB029015

C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)//1.4E-243//584aa//74%//P17812

15 C-PLACE1003915//&quot;PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE- -TRNA LIGASE) (ARGRS).&quot;//2.4E-108//581aa//40%//Q05506

C-PLACE1004118

C-PLACE1004256//&quot;Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.&quot;//2E-93//960bp//76%//AF115778

C-PLACE1004274

20 C-PLACE1004284

C-PLACE1005331

C-PLACE1005739//Homo sapiens mRNA: cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//99%//AL050267

C-PLACE1005828

25 C-PLACE1005876//&quot;CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).&quot;//0//730aa//99%//Q10568

C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%//P54069

C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//30%//P98110

30 C-PLACE1007053

C-PLACE1007068

C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%//Q04652

C-PLACE1009921

35 C-PLACE1010401

C-PLACE1010856

C-PLACE1010857

C-PLACE1010917

C-PLACE1010925

40 C-PLACE1010926//&quot;Homo sapiens mRNA for KIAA0554 protein, partial cds.&quot;//0//1160bp//100%//AB011126

C-PLACE1010942//&quot;Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.&quot;//0//1440bp//99%//AF114487

C-PLACE1010944

45 C-PLACE1010954

C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890

C-PLACE1011026

C-PLACE1011046//&quot;1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).&quot;//0//646aa//97%//P10894

50 C-PLACE1011054

C-PLACE1011057

C-PLACE1011109//&quot;ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).&quot;//1.50E-22//63aa//88%//Q07803

C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//120aa//41%//Q03501

C-PLACE1011115

C-PLACE1011116

C-PLACE1011117

C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100%//P03830

C-PLACE1011219//PROBABLEOXIDOREDUCTASE (EC 1.-.-.-)//3.2E-12//212aa//29%//Q03326  
 C-PLACE1011221  
 C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp564O043)//0//2487bp//  
 99%//AL050390  
 5 C-PLACE1011325  
 C-PLACE1011332//&quot;Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.&quot;//  
 7.2E-151//697bp//99%//AF102265  
 C-PLACE1011340//&quot;Homo sapiens IDN3-B mRNA, complete cds.&quot;//1.20E-74//380bp//97%//  
 AB019602  
 10 C-PLACE1011399//&quot;Homo sapiens CGI-72 protein mRNA, complete cds.&quot;//3.2E-90//427bp//99%//  
 AF151830  
 C-PLACE1011433//&quot;Homo sapiens mRNA for KIAA0530 protein, partial cds.&quot;//0//1946bp//99%//  
 AB011102  
 C-PLACE1011452  
 15 C-PLACE1011465  
 C-PLACE1011472//&quot;Homo sapiens mRNA for KIAA0712 protein, complete cds.&quot;//0//2022bp//99%//  
 AB018255  
 C-PLACE1011477//&quot;Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.&quot;//0//2040bp//99%//  
 AF065482  
 20 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//  
 4.90E-11//147aa//32%//P52178  
 C-PLACE1011520  
 C-PLACE1011563  
 C-PLACE1011567  
 25 C-PLACE1011576//&quot;Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.&quot;//0//  
 1791bp//82%//L11672  
 C-PLACE1011586  
 C-PLACE1011643  
 C-PLACE1011649  
 30 C-PLACE1011664//CROOKED NECK PROTEIN//1.6E-187//505aa//64%//P17886  
 C-PLACE1011682  
 C-PLACE1011719  
 C-PLACE1011729  
 C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021)//0//1490bp//  
 99%//AL050287  
 35 C-PLACE1011874  
 C-PLACE1011875//&quot;Homo sapiens mRNA for KIAA0580 protein, partial cds.&quot;//4.1E-112//524bp//  
 100%//AB011152  
 C-PLACE1011923//&quot;Homo sapiens serum-inducible kinase mRNA, complete cds.&quot;//0//2782bp//99%//  
 40 AF059617  
 C-PLACE1011982  
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//2.6E-42//104aa//49%//  
 Q09475  
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 45 EPS15) (AF-1P PROTEIN)//1.1E-116//364aa//45%//P42566  
 C-PLACE2000017  
 C-PLACE2000021//&quot;Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, com-  
 plete cds.&quot;//2.7E-107//981bp//74%//AF082556  
 C-PLACE2000047  
 50 C-PLACE2000062//&quot;Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type  
 lectin, complete cds, clone:HP01347.&quot;//6.3E-166//656bp//94%//AB015629  
 C-PLACE2000100  
 C-PLACE2000111  
 C-PLACE2000172  
 C-PLACE2000215//&quot;Homo sapiens mRNA for KIAA0795 protein, partial cds.&quot;//4.60E-172//796bp//  
 99%//AB018338

C-PLACE2000317

C-PLACE2000341//&amp;quot;Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.&amp;quot;0//1554bp//99%//AF069307

C-PLACE2000366

5 C-PLACE2000373//F-SPONDIN PRECURSOR.//8.6E-16//371aa//28%//P35446

C-PLACE2000394

C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.3E-37//90aa//98%//P10586

10 C-PLACE2000411//&amp;quot;Homo sapiens mRNA for KIAA1037 protein, partial cds.&amp;quot;0//2515bp//99%//AB028960

C-PLACE2000425

C-PLACE2000427//PROBABLE HELICASE MOT1.//1.2E-26//200aa//27%//P32333

C-PLACE2000433

15 C-PLACE2000438//&amp;quot;POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE)(GALNAC-T1).&amp;quot;2.1E-86//348aa//41%//Q10472

C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.5E-25//165aa//40%//P33450

20 C-PLACE2000477//&amp;quot;Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.&amp;quot;6.7E-127//671bp//94%//AF072733

C-PLACE3000009

C-PLACE3000020//&amp;quot;Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.&amp;quot;0//2253bp//99%//AF033861

C-PLACE3000103

25 C-PLACE3000142

C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205

C-PLACE3000156

C-PLACE3000157

C-PLACE3000197

30 C-PLACE3000208

C-PLACE3000226//&amp;quot;Homo sapiens mRNA for KIAA0962 protein, partial cds.&amp;quot;0//4805bp//99%//AB023179

C-PLACE3000242//&amp;quot;Homo sapiens mRNA for KIAA1114 protein, complete cds.&amp;quot;0//2786bp//96%//AB029037

35 C-PLACE3000363

C-PLACE3000405

C-PLACE3000416//&amp;quot;Homo sapiens mRNA for actin binding protein ABP620, complete cds.&amp;quot;1.80E-141//565bp//98%//AB029290

C-PLACE3000477

40 C-PLACE4000106//&amp;quot;Homo sapiens mRNA for KIAA0462 protein, partial cds.&amp;quot;0//6702bp//99%//AB007931

C-PLACE4000323

C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771

45 C-PLACE4000369//&amp;quot;Homo sapiens mRNA for KIAA1025 protein, partial cds.&amp;quot;0//4830bp//99%//AB028948

C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212).//0//2565bp//99%//AL080196

50 C-PLACE4000558//&amp;quot;Homo sapiens mRNA for KIAA0729 protein, partial cds.&amp;quot;0//1051bp//97%//AB018272

C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.3E-70//226aa//52%//P10079

C-PLACE4000593

C-PLACE4000612//POL POLYPROTEIN (CONTAINS PROTEASE (EC 2.4.22.1), REVERSE TRANSCRIPTASE (EC 2.7.7.7), AND RNA POLYMERASE (EC 2.7.7.6))

C-PLACE400067

C-PLACE4000726

C-THYRO1000085//&amp;quot;PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.&amp;quot;2E-72//155aa//92%//

Q06710

C-THYRO1000107

C-THYRO1000111

C-THYRO1000132//&amp;quot;Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.&amp;quot;//1.1E-159//824bp//95%//U97018

C-THYRO1000156

C-THYRO1000173//&amp;quot;Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.&amp;quot;//0//1713bp//99%//AF020797

C-THYRO1000186

C-THYRO1000187

C-THYRO1000241

C-THYRO1000279

C-THYRO1000327//&amp;quot;Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.&amp;quot;//0//1567bp//99%//AF124145

C-THYRO1000452

C-THYRO1000471

C-THYRO1000484

C-THYRO1000502

C-THYRO1000505

C-THYRO1000585//&amp;quot;Homo sapiens protein associated with Myc mRNA, complete cds.&amp;quot;//0//1901bp//99%//AF075587

C-THYRO1000596

C-THYRO1000662//&amp;quot;Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.&amp;quot;//0//2341 bp//99%//AB024313

C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889

C-THYRO1000715

C-THYRO1000734

C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171

C-THYRO1000756//&amp;quot;ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY).&amp;quot;//1.8E-55//243aa//42%//Q64686

C-THYRO1000777

C-THYRO1000783//&amp;quot;Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.&amp;quot;//2.4E-157//1656bp//70%//U37373

C-THYRO1000787

C-THYRO1000793

C-THYRO1000796

C-THYRO1000843

C-THYRO1000852//&amp;quot;Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene encoding mitochondrial protein, complete cds.&amp;quot;//3.3E-147//790bp//93%//U68418

C-THYRO1000865

C-THYRO1000895

C-THYRO1000926//&amp;quot;Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.&amp;quot;//0//2387bp//99%//AF079529

C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//37%//P43550

C-THYRO1000952

C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132

C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491

C-THYRO1001031

C-THYRO1001062

C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.0E-67//245aa//60%//U68418

C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.0E-67//245aa//60%//U68418

C-THYRO1001173

C-THYRO1001213  
 C-THYRO1001321  
 C-THYRO1001322  
 C-THYRO1001365  
 5 C-THYRO1001401  
 C-THYRO1001411  
 C-THYRO1001434  
 C-THYRO1001534  
 C-THYRO1001541  
 10 C-THYRO1001559  
 C-THYRO1001570  
 C-THYRO1001595  
 C-THYRO1001605  
 C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT)//0//1784bp//  
 15 99%//AJ002190  
 C-THYRO1001656//"Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds."//4.1E-  
 273//1947bp//82%//AF175968  
 C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//0//1820bp//99%//  
 AJ225089  
 20 C-THYRO1001673  
 C-THYRO1001703//NIFR3-LIKE PROTEIN//2.90E-32//282aa//32%//P45672  
 C-THYRO1001706  
 C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL)//2.4E-20//217aa//30%//P38584  
 C-THYRO1001745  
 25 C-THYRO1001793  
 C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF)//1.4E-74//158aa//89%//P42128  
 C-THYRO1001895  
 C-THYRO1001907  
 C-VESEN1000122  
 30 C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1//2.4E-30//80aa//60%//P25916  
 C-Y79AA1000059//"Homo sapiens immunophilin homolog ARA9 mRNA, complete cds."//2.9E-70//  
 1040bp//65%//U78521  
 C-Y79AA1000065  
 C-Y79AA1000131  
 35 C-Y79AA1000181//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//1858bp//99%//  
 AF132936  
 C-Y79AA1000202  
 C-Y79AA1000214//"Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds."//7.1E-71//  
 345bp//100%//AF081192  
 40 C-Y79AA1000230  
 C-Y79AA1000258  
 C-Y79AA1000268//"Mus musculus Nip21 mRNA, complete cds."//2.10E-50//648bp//64%//AF035207  
 C-Y79AA1000313//CALPHOTIN//0.000011//336aa//23%//Q02910  
 C-Y79AA1000328//SEL-10 PROTEIN//0.000000067//219aa//25 %//Q93794  
 45 C-Y79AA1000355  
 C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161//4E-20//261 aa//27%//P25343  
 C-Y79AA1000420  
 C-Y79AA1000469//"Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, com-  
 plete cds."//8.30E-252//1207bp//85%//U41736  
 50 C-Y79AA1000480  
 C-Y79AA1000540  
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 C SUBUNIT)//0//652aa//98%//P17427  
 C-Y79AA1000627//"Homo sapiens 14-3-3 protein gamma mRNA, complete cds."//1.1E-70//  
 1040bp//82%//AF060503  
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1//5.80E-254//1477bp//84%//X69942

C-Y79AA1000734//&quot;Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.&quot;//  
 0//1594bp//99%//AF093670  
 C-Y79AA1000748//&quot;Homo sapiens CGI-05 protein mRNA, complete cds.&quot;//1.9E-239//1367bp//91%//  
 AF152097  
 5 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP)//  
 4.9E-91//200aa//64%//Q61990  
 C-Y79AA1000774  
 C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5)//3E-37//469aa//27%//P49902  
 C-Y79AA1000784//&quot;Homo sapiens RanBP7/importin 7 mRNA, complete cds.&quot;//1.10E-236//1076bp//  
 99%//AF098799  
 10 C-Y79AA1000794//&quot;Homo sapiens actin-associated protein 2E4/kaptein (2E4) mRNA, 2E4-1 allele, complete  
 cds.&quot;//0//1610bp//99%//AF105369  
 C-Y79AA1000800//&quot;Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.&quot;//1.6E-  
 284//1288bp//99%//AF072733  
 15 C-Y79AA1000805  
 C-Y79AA1000824  
 C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN//5E-173//220aa//79%//P05209  
 C-Y79AA1000850  
 C-Y79AA1000962//&quot;MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)&quot;//  
 4.2E-17//430aa//27%//Q99323  
 20 C-Y79AA1000968//&quot;Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, com-  
 plete cds.&quot;//3.9E-248//1468bp//87%//U38253  
 C-Y79AA1000976  
 C-Y79AA1001023  
 25 C-Y79AA1001041  
 C-Y79AA1001048//&quot;ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC  
 1.3.99.-) (VLCAD)&quot;//3.1E-138//583aa//47%//P45953  
 C-Y79AA1001077  
 C-Y79AA1001078  
 30 C-Y79AA1001145  
 C-Y79AA1001177  
 C-Y79AA1001185  
 C-Y79AA1001211//&quot;Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.&quot;//  
 0//1435bp//99%//AF139658  
 35 C-Y79AA1001228  
 C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-  
 DROXYSTEROID DEHYDROGENASE 1)//7.7E-50//228aa//42%//P51657  
 C-Y79AA1001236//&quot;Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581  
 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).&quot;//0//1653bp//99%//AJ005892  
 40 C-Y79AA1001281  
 C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46)//0.000000023//193aa//30%//  
 Q03309  
 C-Y79AA1001323//&quot;Mus musculus mRNA for GSG1, complete cds.&quot;//3.3E-172//1171bp//83%//  
 D87325  
 45 C-Y79AA1001391//HOMEODOMAIN PROTEIN HOX-A13 (HOX-1J)//1.2E-58//178aa//66%//P31271  
 C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-)//1.2E-13//230aa//32%//O83746  
 C-Y79AA1001402//&quot;Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.  
 &quot;//8.50E-65//784bp//62%//AF083115  
 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN  
 50 LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)//3.80E-18//151aa//38%//P35132  
 C-Y79AA1001533//&quot;Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.&quot;//  
 4.5E-193//1333bp//80%//D14336  
 C-Y79AA1001541  
 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4 KINASE) (PTDINS 4-K  
 INASE) (PI4K) (PDK1) (PDK1A) (PDK1B) (PDK1C) (PDK1D) (PDK1E) (PDK1F) (PDK1G) (PDK1H) (PDK1I) (PDK1J)  
 (PDK1K) (PDK1L) (PDK1M) (PDK1N) (PDK1O) (PDK1P) (PDK1Q) (PDK1R) (PDK1S) (PDK1T) (PDK1U) (PDK1V)  
 (PDK1W) (PDK1X) (PDK1Y) (PDK1Z) (PDK1AA) (PDK1AB) (PDK1AC) (PDK1AD) (PDK1AE) (PDK1AF) (PDK1AG)  
 (PDK1AH) (PDK1AI) (PDK1AJ) (PDK1AK) (PDK1AL) (PDK1AM) (PDK1AN) (PDK1AO) (PDK1AP) (PDK1AQ) (PDK1AR)  
 (PDK1AS) (PDK1AT) (PDK1AU) (PDK1AV) (PDK1AW) (PDK1AX) (PDK1AY) (PDK1AZ) (PDK1BA) (PDK1BB) (PDK1BC)  
 (PDK1BD) (PDK1BE) (PDK1BF) (PDK1BG) (PDK1BH) (PDK1BI) (PDK1BJ) (PDK1BK) (PDK1BL) (PDK1BM) (PDK1BN)  
 (PDK1BO) (PDK1BP) (PDK1BQ) (PDK1BR) (PDK1BS) (PDK1BT) (PDK1BU) (PDK1BV) (PDK1BW) (PDK1BX) (PDK1BY)  
 (PDK1BZ) (PDK1CA) (PDK1CB) (PDK1CC) (PDK1CD) (PDK1CE) (PDK1CF) (PDK1CG) (PDK1CH) (PDK1CI) (PDK1CJ)  
 (PDK1CK) (PDK1CL) (PDK1CM) (PDK1CN) (PDK1CO) (PDK1CP) (PDK1CQ) (PDK1CR) (PDK1CS) (PDK1CT) (PDK1CU)  
 (PDK1CV) (PDK1CW) (PDK1CX) (PDK1CY) (PDK1CZ) (PDK1DA) (PDK1DB) (PDK1DC) (PDK1DD) (PDK1DE) (PDK1DF)  
 (PDK1DG) (PDK1DH) (PDK1DI) (PDK1DJ) (PDK1DK) (PDK1DL) (PDK1DM) (PDK1DN) (PDK1DO) (PDK1DP) (PDK1DQ)  
 (PDK1DR) (PDK1DS) (PDK1DT) (PDK1DU) (PDK1DV) (PDK1DW) (PDK1DX) (PDK1DY) (PDK1DZ) (PDK1EA) (PDK1EB)  
 (PDK1EC) (PDK1ED) (PDK1EE) (PDK1EF) (PDK1EG) (PDK1EH) (PDK1EI) (PDK1EJ) (PDK1EK) (PDK1EL) (PDK1EM)  
 (PDK1EN) (PDK1EO) (PDK1EP) (PDK1EQ) (PDK1ER) (PDK1ES) (PDK1ET) (PDK1EU) (PDK1EV) (PDK1EW) (PDK1EX)  
 (PDK1EY) (PDK1EZ) (PDK1FA) (PDK1FB) (PDK1FC) (PDK1FD) (PDK1FE) (PDK1FF) (PDK1FG) (PDK1FH) (PDK1FI)  
 (PDK1FJ) (PDK1FK) (PDK1FL) (PDK1FM) (PDK1FN) (PDK1FO) (PDK1FP) (PDK1FQ) (PDK1FR) (PDK1FS) (PDK1FT)  
 (PDK1FU) (PDK1FV) (PDK1FW) (PDK1FX) (PDK1FY) (PDK1FZ) (PDK1GA) (PDK1GB) (PDK1GC) (PDK1GD) (PDK1GE)  
 (PDK1GF) (PDK1GG) (PDK1GH) (PDK1GI) (PDK1GJ) (PDK1GK) (PDK1GL) (PDK1GM) (PDK1GN) (PDK1GO) (PDK1GP)  
 (PDK1GQ) (PDK1GR) (PDK1GS) (PDK1GT) (PDK1GU) (PDK1GV) (PDK1GW) (PDK1GX) (PDK1GY) (PDK1GZ) (PDK1HA)  
 (PDK1HB) (PDK1HC) (PDK1HD) (PDK1HE) (PDK1HF) (PDK1HG) (PDK1HH) (PDK1HI) (PDK1HJ) (PDK1HK) (PDK1HL)  
 (PDK1HM) (PDK1HN) (PDK1HO) (PDK1HP) (PDK1HQ) (PDK1HR) (PDK1HS) (PDK1HT) (PDK1HU) (PDK1HV) (PDK1HW)  
 (PDK1HX) (PDK1HY) (PDK1HZ) (PDK1IA) (PDK1IB) (PDK1IC) (PDK1ID) (PDK1IE) (PDK1IF) (PDK1IG) (PDK1IH)  
 (PDK1IJ) (PDK1IK) (PDK1IL) (PDK1IM) (PDK1IN) (PDK1IO) (PDK1IP) (PDK1IQ) (PDK1IR) (PDK1IS) (PDK1IT)  
 (PDK1IU) (PDK1IV) (PDK1IW) (PDK1IX) (PDK1IY) (PDK1IZ) (PDK1JA) (PDK1JB) (PDK1JC) (PDK1JD) (PDK1JE)  
 (PDK1JF) (PDK1JG) (PDK1JH) (PDK1JI) (PDK1JJ) (PDK1JK) (PDK1JL) (PDK1JM) (PDK1JN) (PDK1JO) (PDK1JP)  
 (PDK1JQ) (PDK1JR) (PDK1JS) (PDK1JT) (PDK1JU) (PDK1JV) (PDK1JW) (PDK1JX) (PDK1JY) (PDK1JZ) (PDK1KA)  
 (PDK1KB) (PDK1KC) (PDK1KD) (PDK1KE) (PDK1KF) (PDK1KG) (PDK1KH) (PDK1KI) (PDK1KJ) (PDK1KK) (PDK1KL)  
 (PDK1KM) (PDK1KN) (PDK1KO) (PDK1KP) (PDK1KQ) (PDK1KR) (PDK1KS) (PDK1KT) (PDK1KU) (PDK1KV) (PDK1KW)  
 (PDK1KX) (PDK1KY) (PDK1KZ) (PDK1LA) (PDK1LB) (PDK1LC) (PDK1LD) (PDK1LE) (PDK1LF) (PDK1LG) (PDK1LH)  
 (PDK1LI) (PDK1LJ) (PDK1LK) (PDK1LL) (PDK1LM) (PDK1LN) (PDK1LO) (PDK1LP) (PDK1LQ) (PDK1LR) (PDK1LS)  
 (PDK1LT) (PDK1LU) (PDK1LV) (PDK1LW) (PDK1LX) (PDK1LY) (PDK1LZ) (PDK1MA) (PDK1MB) (PDK1MC) (PDK1MD)  
 (PDK1ME) (PDK1MF) (PDK1MG) (PDK1MH) (PDK1MI) (PDK1MJ) (PDK1MK) (PDK1ML) (PDK1MN) (PDK1MO) (PDK1MP)  
 (PDK1MQ) (PDK1MR) (PDK1MS) (PDK1MT) (PDK1MU) (PDK1MV) (PDK1MW) (PDK1MX) (PDK1MY) (PDK1MZ) (PDK1NA)  
 (PDK1NB) (PDK1NC) (PDK1ND) (PDK1NE) (PDK1NF) (PDK1NG) (PDK1NH) (PDK1NI) (PDK1NJ) (PDK1NK) (PDK1NL)  
 (PDK1NM) (PDK1NO) (PDK1NP) (PDK1NQ) (PDK1NR) (PDK1NS) (PDK1NT) (PDK1NU) (PDK1NV) (PDK1NW) (PDK1NX)  
 (PDK1NY) (PDK1NZ) (PDK1OA) (PDK1OB) (PDK1OC) (PDK1OD) (PDK1OE) (PDK1OF) (PDK1OG) (PDK1OH) (PDK1OI)  
 (PDK1OJ) (PDK1OK) (PDK1OL) (PDK1OM) (PDK1ON) (PDK1OO) (PDK1OP) (PDK1OQ) (PDK1OR) (PDK1OS) (PDK1OT)  
 (PDK1OU) (PDK1OV) (PDK1OW) (PDK1OX) (PDK1OY) (PDK1OZ) (PDK1PA) (PDK1PB) (PDK1PC) (PDK1PD) (PDK1PE)  
 (PDK1PF) (PDK1PG) (PDK1PH) (PDK1PI) (PDK1PJ) (PDK1PK) (PDK1PL) (PDK1PM) (PDK1PN) (PDK1PO) (PDK1PP)  
 (PDK1PQ) (PDK1PR) (PDK1PS) (PDK1PT) (PDK1PU) (PDK1PV) (PDK1PW) (PDK1PX) (PDK1PY) (PDK1PZ) (PDK1QA)  
 (PDK1QB) (PDK1QC) (PDK1QD) (PDK1QE) (PDK1QF) (PDK1QG) (PDK1QH) (PDK1QI) (PDK1QJ) (PDK1QK) (PDK1QL)  
 (PDK1QM) (PDK1QN) (PDK1QO) (PDK1QP) (PDK1QQ) (PDK1QR) (PDK1QS) (PDK1QT) (PDK1QU) (PDK1QV) (PDK1QW)  
 (PDK1QX) (PDK1QY) (PDK1QZ) (PDK1RA) (PDK1RB) (PDK1RC) (PDK1RD) (PDK1RE) (PDK1RF) (PDK1RG) (PDK1RH)  
 (PDK1RI) (PDK1RJ) (PDK1RK) (PDK1RL) (PDK1RM) (PDK1RN) (PDK1RO) (PDK1RP) (PDK1RQ) (PDK1RR) (PDK1RS)  
 (PDK1RT) (PDK1RU) (PDK1RV) (PDK1RW) (PDK1RX) (PDK1RY) (PDK1RZ) (PDK1SA) (PDK1SB) (PDK1SC) (PDK1SD)  
 (PDK1SE) (PDK1SF) (PDK1SG) (PDK1SH) (PDK1SI) (PDK1SJ) (PDK1SK) (PDK1SL) (PDK1SM) (PDK1SN) (PDK1SO)  
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 25 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5E-163//752bp//99%//X86018  
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 35 C-Y79AA1002298  
 C-Y79AA1002307//&quot;Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.&quot;//0//1209bp//99%//  
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 C-Y79AA1002433//&quot;Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit  
 mRNA, complete cds.&quot;//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5E-136//472aa//  
 45 49%//Q05481

## Homology Search Result Data 13.

[0333] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequenc-  
 50 es. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,  
 and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000042

C-HEMBA1000141//Homo sapiens SUMO1-specific protease, SSBP1 mRNA, complete cds.

C-HEMBA1000141//Homo sapiens SUMO1-specific protease, SSBP1 mRNA, complete cds.

C-HEMBA1000141//Homo sapiens SUMO1-specific protease, SSBP1 mRNA, complete cds.

C-HEMBA1000213

C-HEMBA1000243

C-HEMBA1000244  
 C-HEMBA1000251  
 C-HEMBA1000338  
 C-HEMBA1000357  
 5 C-HEMBA1000376  
 C-HEMBA1000428  
 C-HEMBA1000469  
 C-HEMBA1000497  
 10 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//  
 25%//Q05481  
 C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%//Q60865  
 C-HEMBA1000575  
 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246  
 C-HEMBA1000673  
 15 C-HEMBA1000702  
 C-HEMBA1000722  
 C-HEMBA1000726  
 C-HEMBA1000876  
 C-HEMBA1000942  
 20 C-HEMBA1000943  
 C-HEMBA1000960  
 C-HEMBA1000985  
 C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE)  
 (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493  
 25 C-HEMBA1001020  
 C-HEMBA1001024  
 C-HEMBA1001026  
 C-HEMBA1001051  
 C-HEMBA1001060  
 30 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSORS.//1.50E-92//82aa//100%//P02461  
 C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//  
 432bp//94%//AF119043  
 C-HEMBA1001099  
 C-HEMBA1001121  
 35 C-HEMBA1001123  
 C-HEMBA1001208  
 C-HEMBA1001213  
 C-HEMBA1001226  
 C-HEMBA1001247  
 40 C-HEMBA1001299  
 C-HEMBA1001319  
 C-HEMBA1001323  
 C-HEMBA1001327  
 C-HEMBA1001361  
 45 C-HEMBA1001375  
 C-HEMBA1001377  
 C-HEMBA1001383  
 C-HEMBA1001391  
 C-HEMBA1001411  
 50 C-HEMBA1001432  
 C-HEMBA1001433  
 C-HEMBA1001435  
 C-HEMBA1001442  
 C-HEMBA1001463  
 C-HEMBA1001521  
 C-HEMBA1001551  
 C-HEMBA1001566

C-HEMBA1001589  
 C-HEMBA1001608  
 C-HEMBA1001636  
 C-HEMBA1001647  
 5 C-HEMBA1001651  
 C-HEMBA1001658  
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//  
 P54787  
 C-HEMBA1001712  
 10 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//  
 1.10E-38//87aa//96%//P55288  
 C-HEMBA1001745  
 C-HEMBA1001750  
 C-HEMBA1001784  
 15 C-HEMBA1001791  
 C-HEMBA1001803  
 C-HEMBA1001820  
 C-HEMBA1001835  
 C-HEMBA1001888  
 20 C-HEMBA1001912  
 C-HEMBA1001915  
 C-HEMBA1001918  
 C-HEMBA1001940  
 C-HEMBA1001942  
 25 C-HEMBA1001964  
 C-HEMBA1002022  
 C-HEMBA1002039  
 C-HEMBA1002100  
 C-HEMBA1002113  
 30 C-HEMBA1002119  
 C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847  
 C-HEMBA1002160  
 C-HEMBA1002162  
 C-HEMBA1002166  
 35 C-HEMBA1002185  
 C-HEMBA1002204  
 C-HEMBA1002328  
 C-HEMBA1002337  
 C-HEMBA1002348  
 40 C-HEMBA1002381  
 C-HEMBA1002486  
 C-HEMBA1002498  
 C-HEMBA1002538  
 C-HEMBA1002552  
 45 C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//  
 68%//AF055993  
 C-HEMBA1002558  
 C-HEMBA1002621  
 C-HEMBA1002629  
 50 C-HEMBA1002645  
 C-HEMBA1002659  
 C-HEMBA1002661  
 C-HEMBA1002666  
 C-HEMBA1002678  
 C-HEMBA1002711  
 C-HEMBA1002716  
 C-HEMBA1002742

# EP 1 074 617 A2

C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7)//5.00E-37//268aa//34%//P06746  
 C-HEMBA1002748  
 C-HEMBA1002780  
 C-HEMBA1002801  
 5 C-HEMBA1002826  
 C-HEMBA1002833  
 C-HEMBA1002921  
 C-HEMBA1002934  
 C-HEMBA1002944  
 10 C-HEMBA1002968  
 C-HEMBA1003034  
 C-HEMBA1003037  
 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN  
 PRECURSOR (ALS)//1.30E-09//121aa//40%//P35858  
 15 C-HEMBA1003078  
 C-HEMBA1003083  
 C-HEMBA1003086  
 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds//6.20E-273//1253bp//99%//AF155096  
 C-HEMBA1003133  
 20 C-HEMBA1003142  
 C-HEMBA1003166  
 C-HEMBA1003197  
 C-HEMBA1003202  
 C-HEMBA1003220  
 25 C-HEMBA1003229  
 C-HEMBA1003276  
 C-HEMBA1003278  
 C-HEMBA1003328  
 C-HEMBA1003373  
 30 C-HEMBA1003597  
 C-HEMBA1003598  
 C-HEMBA1003656  
 C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-)//2.40E-92//  
 423aa//47%//P34629  
 35 C-HEMBA1003733  
 C-HEMBA1003742  
 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)  
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA)//3.70E-124//347aa//55%//Q16665  
 C-HEMBA1003803  
 40 C-HEMBA1003854  
 C-HEMBA1003926  
 C-HEMBA1003939  
 C-HEMBA1003987  
 C-HEMBA1004012  
 45 C-HEMBA1004015  
 C-HEMBA1004193  
 C-HEMBA1004225  
 C-HEMBA1004241  
 C-HEMBA1004267  
 50 C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds//9.40E-31//381bp//65%//AF155103  
 C-HEMBA1004354//CHL1 PROTEIN//9.90E-26//130aa//42%//P22516  
 C-HEMBA1004356//H.sapiens MSSP-2 mRNA//3.00E-243//573bp//98%//X77494  
 C-HEMBA1004396  
 C-HEMBA1004405  
 C-HEMBA1004450  
 C-HEMBA1004542  
 C-HEMBA1004573

C-HEMBA1004577  
 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844  
 C-HEMBA1004617  
 C-HEMBA1004631  
 5 C-HEMBA1004705  
 C-HEMBA1004733  
 C-HEMBA1004748  
 C-HEMBA1004778  
 C-HEMBA1004803  
 10 C-HEMBA1004807  
 C-HEMBA1004820  
 C-HEMBA1004865  
 C-HEMBA1004880  
 C-HEMBA1004900  
 15 C-HEMBA1004909  
 C-HEMBA1004960  
 C-HEMBA1004978  
 C-HEMBA1004980  
 C-HEMBA1004983  
 20 C-HEMBA1004995  
 C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2212bp//99%//AB014548  
 C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947  
 C-HEMBA1005035  
 C-HEMBA1005039  
 25 C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16)//3.40E-101//106aa//98%//P35290  
 C-HEMBA1005050  
 C-HEMBA1005062  
 C-HEMBA1005066  
 C-HEMBA1005075  
 30 C-HEMBA1005079  
 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//  
 AF080561  
 C-HEMBA1005123  
 C-HEMBA1005149  
 35 C-HEMBA1005152  
 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941  
 C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)//1.90E-179//361aa//95%//  
 Q00004  
 C-HEMBA1005223  
 40 C-HEMBA1005232  
 C-HEMBA1005241  
 C-HEMBA1005275  
 C-HEMBA1005293  
 C-HEMBA1005311  
 45 C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581  
 C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743  
 C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//  
 AF071787  
 C-HEMBA1005374  
 50 C-HEMBA1005382  
 C-HEMBA1005411  
 C-HEMBA1005426  
 C-HEMBA1005443  
 C-HEMBA1005447  
 C-HEMBA1005450  
 C-HEMBA1005500  
 C-HEMBA1005506  
 C-HEMBA1005508

C-HEMBA1005526

C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//1578bp//98%//AF191340

C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%//AF134157

C-HEMBA1005552

C-HEMBA1005568

C-HEMBA1005588

C-HEMBA1005593

C-HEMBA1005606

C-HEMBA1005616

C-HEMBA1005627

C-HEMBA1005670

C-HEMBA1005679

C-HEMBA1005699

C-HEMBA1005705

C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//317bp//98%//D14697

C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789

C-HEMBA1005852

C-HEMBA1005894

C-HEMBA1005921

C-HEMBA1006035

C-HEMBA1006036

C-HEMBA1006090

C-HEMBA1006138

C-HEMBA1006173

C-HEMBA1006252

C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836

C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//1.60E-130//332aa//62%//002193

C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160

C-HEMBA1006380

C-HEMBA1006416

C-HEMBA1006421

C-HEMBA1006424

C-HEMBA1006426

C-HEMBA1006446

C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%//P55786

C-HEMBA1006486

C-HEMBA1006494

C-HEMBA1006546

C-HEMBA1006562

C-HEMBA1006595

C-HEMBA1006597

C-HEMBA1006631

C-HEMBA1006639

C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148

C-HEMBA1006659

C-HEMBA1006665

C-HEMBA1006676

C-HEMBA1006695

C-HEMBA1006709

C-HEMBA1006758//Homo sapiens protocadherin beta 12 (PCDH beta 12) mRNA, complete cds.//1.00E-220//1014bp//99%//AF134157

C-HEMBA1006788

C-HEMBA1006807//Homo sapiens mRNA for SPDP.//5.70E-125//1109bp//75%//AJ000644

C-HEMBA1006824

C-HEMBA1006865  
 C-HEMBA1006921  
 C-HEMBA1006949  
 5 C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//  
 447bp//89%/X74570  
 C-HEMBA1007051  
 C-HEMBA1007052  
 C-HEMBA1007066  
 C-HEMBA1007073  
 10 C-HEMBA1007078  
 C-HEMBA1007085  
 C-HEMBA1007113  
 C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//  
 92%/AF125042  
 15 C-HEMBA1007129  
 C-HEMBA1007147  
 C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%/AF076929  
 C-HEMBA1007178  
 C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//1212bp//98%/D86987  
 20 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%/  
 AF196304  
 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%/J00060  
 C-HEMBA1007251  
 C-HEMBA1007288  
 25 C-HEMBA1007322  
 C-HEMBA1007341  
 C-HEMBB1000050  
 C-HEMBB1000054  
 C-HEMBB1000059  
 30 C-HEMBB1000089  
 C-HEMBB1000113  
 C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLA-  
 SE ACTIVATOR PROTEIN P24)//1.40E-24//71aa//77%/P51177  
 C-HEMBB1000173  
 35 C-HEMBB1000175  
 C-HEMBB1000272  
 C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%/P37888  
 C-HEMBB1000318  
 C-HEMBB1000336  
 40 C-HEMBB1000341  
 C-HEMBB1000343  
 C-HEMBB1000354  
 C-HEMBB1000374  
 C-HEMBB1000434  
 45 C-HEMBB1000441  
 C-HEMBB1000491  
 C-HEMBB1000493  
 C-HEMBB1000510  
 C-HEMBB1000652  
 50 C-HEMBB1000672  
 C-HEMBB1000684  
 C-HEMBB1000709  
 C-HEMBB1000726  
 C-HEMBB1000770  
 C-HEMBB1000881  
 C-HEMBB1000883  
 C-HEMBB1000888

C-HEMBB1000893  
 C-HEMBB1000913  
 C-HEMBB1000996  
 C-HEMBB1001004  
 5 C-HEMBB1001047  
 C-HEMBB1001060  
 C-HEMBB1001114  
 C-HEMBB1001119  
 C-HEMBB1001133  
 10 C-HEMBB1001142  
 C-HEMBB1001177  
 C-HEMBB1001208  
 C-HEMBB1001209  
 C-HEMBB1001249  
 15 C-HEMBB1001253  
 C-HEMBB1001254  
 C-HEMBB1001271  
 C-HEMBB1001304  
 C-HEMBB1001317  
 20 C-HEMBB1001348  
 C-HEMBB1001394  
 C-HEMBB1001410  
 C-HEMBB1001424  
 C-HEMBB1001426  
 25 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001436  
 C-HEMBB10014437/Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 C-HEMBB1001449  
 30 C-HEMBB1001458  
 C-HEMBB1001521  
 C-HEMBB1001531  
 C-HEMBB1001535  
 C-HEMBB1001536  
 35 C-HEMBB1001564  
 C-HEMBB1001565  
 C-HEMBB1001585  
 C-HEMBB1001588  
 C-HEMBB1001603  
 40 C-HEMBB1001618  
 C-HEMBB1001635  
 C-HEMBB1001653  
 C-HEMBB1001668  
 C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0//2035bp//99%//AB014546  
 45 C-HEMBB1001685  
 C-HEMBB1001695  
 C-HEMBB1001707  
 C-HEMBB1001735  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 50 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001747  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001753  
 C-HEMBB1001756  
 C-HEMBB1001757  
 C-HEMBB1001758  
 C-HEMBB1001759  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167

C-HEMBB1001816  
 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 5 P18720  
 C-HEMBB1001850  
 C-HEMBB1001863  
 C-HEMBB1001868  
 C-HEMBB1001874  
 10 C-HEMBB1001880  
 C-HEMBB1001899  
 C-HEMBB1001906  
 C-HEMBB1001910  
 C-HEMBB1001911  
 15 C-HEMBB1001921  
 C-HEMBB1001922  
 C-HEMBB1001930  
 C-HEMBB1001944  
 C-HEMBB1001945  
 20 C-HEMBB1001947  
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)  
 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEMBB1001952  
 C-HEMBB1001957  
 25 C-HEMBB1001962  
 C-HEMBB1001983  
 C-HEMBB1001990  
 C-HEMBB1001996  
 C-HEMBB1002002  
 30 C-HEMBB1002005  
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.70E-49//139aa//55%//P29981  
 C-HEMBB1002043  
 C-HEMBB1002045  
 C-HEMBB1002049  
 35 C-HEMBB1002050  
 C-HEMBB1002068  
 C-HEMBB1002092  
 C-HEMBB1002139  
 C-HEMBB1002142  
 40 C-HEMBB1002190  
 C-HEMBB1002193  
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEMBB1002218  
 45 C-HEMBB1002232  
 C-HEMBB1002247  
 C-HEMBB1002249  
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEMBB1002327  
 50 C-HEMBB1002329  
 C-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%//  
 AJ010841  
 C-HEMBB1002358  
 C-HEMBB1002371  
 C-HEMBB1002373  
 C-HEMBB1002400  
 C-HEMBB1002420  
 C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692

C-HEMBB1002453  
 C-HEMBB1002458  
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885  
 C-HEMBB1002489  
 5 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365  
 C-HEMBB1002520  
 C-HEMBB1002522  
 C-HEMBB1002545  
 C-HEMBB1002579  
 10 C-HEMBB1002582  
 C-HEMBB1002596  
 C-HEMBB1002603  
 C-HEMBB1002610  
 C-HEMBB1002613  
 15 C-HEMBB1002617  
 C-HEMBB1002623  
 C-HEMBB1002635  
 C-HEMBB1002677  
 C-HEMBB1002683  
 20 C-HEMBB1002699  
 C-HEMBB1002702  
 C-MAMMA1000009  
 C-MAMMA1000043  
 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN  
 25 GP37].//1.90E-07//249aa//27%//P03396  
 C-MAMMA1000057  
 C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--  
 TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860  
 C-MAMMA1000092  
 30 C-MAMMA1000103  
 C-MAMMA1000117  
 C-MAMMA1000129  
 C-MAMMA1000133  
 C-MAMMA1000155  
 35 C-MAMMA1000175  
 C-MAMMA1000198  
 C-MAMMA1000241  
 C-MAMMA1000251  
 C-MAMMA1000254  
 40 C-MAMMA1000287  
 C-MAMMA1000307  
 C-MAMMA1000331  
 C-MAMMA1000339  
 C-MAMMA1000340  
 45 C-MAMMA1000348  
 C-MAMMA1000356  
 C-MAMMA1000360  
 C-MAMMA1000402  
 C-MAMMA1000414  
 50 C-MAMMA1000431  
 C-MAMMA1000444  
 C-MAMMA1000458  
 C-MAMMA1000500  
 C-MAMMA1000522  
 C-MAMMA1000550  
 C-MAMMA1000558  
 C-MAMMA1000594  
 C-MAMMA1000605

C-MAMMA1000616

C-MAMMA1000643

C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds.//0//2402bp//99%//AF109134

C-MAMMA1000696

5 C-MAMMA1000707

C-MAMMA1000714

C-MAMMA1000720

C-MAMMA1000744

C-MAMMA1000761

10 C-MAMMA1000776

C-MAMMA1000798

C-MAMMA1000839

C-MAMMA1000851

C-MAMMA1000863

15 C-MAMMA1000867

C-MAMMA1000876

C-MAMMA1000880

C-MAMMA1000883

C-MAMMA1000921

20 C-MAMMA1000931

C-MAMMA1000941

C-MAMMA1000957

C-MAMMA1000962

C-MAMMA1000975

25 C-MAMMA1000987

C-MAMMA1001003

C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674

30 C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746

C-MAMMA1001082

C-MAMMA1001162

C-MAMMA1001186

C-MAMMA1001191

35 C-MAMMA1001206

C-MAMMA1001220

C-MAMMA1001243

C-MAMMA1001249

C-MAMMA1001256

40 C-MAMMA1001268

C-MAMMA1001271

C-MAMMA1001274

C-MAMMA1001292

45 C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960

C-MAMMA1001324

C-MAMMA1001341

50 C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750

C-MAMMA1001397

C-MAMMA1001408

C-MAMMA1001420

C-MAMMA1001442

C-MAMMA1001452

C-MAMMA1001478

C-MAMMA1001498

C-MAMMA1001501//CALPAIN I, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

C-MAMMA1001547  
 C-MAMMA1001551  
 C-MAMMA1001575  
 C-MAMMA1001590  
 5 C-MAMMA1001600  
 C-MAMMA1001606  
 C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989  
 C-MAMMA1001663  
 C-MAMMA1001670  
 10 C-MAMMA1001671  
 C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ)//0.00000058//29aa//100%//P47756  
 C-MAMMA1001711  
 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V)//5.90E-240//445aa//97%//P09653  
 C-MAMMA1001744  
 15 C-MAMMA1001745  
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete  
 cds.//0//2332bp//99%//AF117708  
 C-MAMMA1001783  
 C-MAMMA1001788  
 20 C-MAMMA1001806  
 C-MAMMA1001812  
 C-MAMMA1001815  
 C-MAMMA1001817  
 C-MAMMA1001818  
 25 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148  
 C-MAMMA1001824  
 C-MAMMA1001851  
 C-MAMMA1001854  
 C-MAMMA1001864  
 30 C-MAMMA1001878  
 C-MAMMA1001890  
 C-MAMMA1001907  
 C-MAMMA1001908  
 C-MAMMA1001931  
 35 C-MAMMA1001969  
 C-MAMMA1002011  
 C-MAMMA1002032  
 C-MAMMA1002041  
 C-MAMMA1002047  
 40 C-MAMMA1002056  
 C-MAMMA1002058  
 C-MAMMA1002078  
 C-MAMMA1002082  
 C-MAMMA1002084  
 45 C-MAMMA1002093  
 C-MAMMA1002094  
 C-MAMMA1002118  
 C-MAMMA1002125  
 C-MAMMA1002132  
 50 C-MAMMA1002140  
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds//1.70E-252//1170bp//99%//  
 AF099664  
 C-MAMMA1002145  
 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN DEPENDENT PEROXIDE REDUCTASE)  
 THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN DEPENDENT PEROXIDE REDUCTASE)  
 C-MAMMA1002200  
 C-MAMMA1002250

C-MAMMA1002282  
 C-MAMMA1002293  
 C-MAMMA1002298  
 C-MAMMA1002299  
 5 C-MAMMA1002308  
 C-MAMMA1002310  
 C-MAMMA1002311  
 C-MAMMA1002322  
 C-MAMMA1002339  
 10 C-MAMMA1002352  
 C-MAMMA1002359  
 C-MAMMA1002360  
 C-MAMMA1002392  
 C-MAMMA1002411  
 15 C-MAMMA1002413  
 C-MAMMA1002417  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE  
 SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2)//1.10E-24//96aa//68%//Q14108  
 C-MAMMA1002434  
 20 C-MAMMA1002446  
 C-MAMMA1002454  
 C-MAMMA1002461  
 C-MAMMA1002475  
 C-MAMMA1002556  
 25 C-MAMMA1002566  
 C-MAMMA1002612  
 C-MAMMA1002622//VILLIN//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC)//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds//5.40E-57//480bp//68%//AF194030  
 30 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds//4.3e-317//  
 1942bp//85%//AF018261  
 C-MAMMA1002727  
 C-MAMMA1002748  
 C-MAMMA1002758  
 35 C-MAMMA1002780  
 C-MAMMA1002820  
 C-MAMMA1002833  
 C-MAMMA1002843  
 C-MAMMA1002895  
 40 C-MAMMA1002937//ZINC FINGER PROTEIN 135//8.30E-99//393aa//43%//P52742  
 C-MAMMA1003004  
 C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds//0//  
 1533bp//99%//AF077952  
 C-NT2RM1000001//D.melanogaster sap47-2 mRNA//1.50E-10//417bp//62%//X80110  
 45 C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//0//3376bp//99%//D31886  
 C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//0//3551bp//99%//AB014590  
 C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//0//3035bp//96%//AB014561  
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR//4.40E-21//372aa//30%//P10775 C-NT2RM1000499  
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4//3.60E-11//180aa//28%//  
 50 Q99383  
 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//3.60E-115//332aa//  
 52%//Q05481  
 C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds//0//3471bp//99%//AB028990  
 C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//0//3553bp//99%//AB014590  
 C-NT2RM2001636//Homo sapiens mRNA for KIAA0618 protein, complete cds//0//3553bp//99%//AB014590  
 C-NT2RM2001637//Homo sapiens mRNA for KIAA0618 protein, complete cds//0//3553bp//99%//AB014590  
 C-NT2RM2001638//Homo sapiens mRNA for KIAA0618 protein, complete cds//0//3553bp//99%//AB014590  
 C-NT2RM2001639//Homo sapiens mRNA for KIAA0618 protein, complete cds//0//3553bp//99%//AB014590  
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-291) //6.50E-104//407aa//43%//Q07230  
 C-NT2RM2001699

C-NT2RM2001706  
 C-NT2RM2001718  
 C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2892bp//99%//AB007931  
 C-NT2RM2001805  
 5 C-NT2RM4000086  
 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962  
 C-NT2RM4000414  
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652  
 C-NT2RM4000634  
 10 C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//0//1412bp//100%//AB028992  
 C-NT2RM4000783  
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750  
 C-NT2RM4000971  
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//  
 15 50%//Q05481  
 C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%//P38682  
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532  
 C-NT2RM4001569  
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//  
 20 8.10E-300//1395bp//98%//M37712  
 C-NT2RM4001905  
 C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//0//2234bp//99%//AB020705  
 C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//  
 1.90E-31//80aa//52%//P36419  
 25 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//  
 AF072758  
 C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//  
 2550bp//99%//AF176085  
 C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2572bp//99%//  
 30 AF071592  
 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940  
 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430  
 C-NT2RM4002390  
 C-NT2RM4002398  
 35 C-NT2RM4002420  
 C-NT2RM4002534  
 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962  
 C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//  
 4.60E-78//921bp//69%//X85019  
 40 C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp//  
 88%//AL050019  
 C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
 ZYME 1).//8.20E-83//345aa//47%//Q61068  
 45 C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//  
 99%//AL050118  
 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
 PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721  
 C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//  
 50 1687bp//99%//AF145020  
 C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//  
 98%//AF047020  
 C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094  
 C-NT2RP1000916  
 C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001113

C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146)//0//2333bp//99%//AL080222

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139

C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513

C-NT2RP1001311

C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799

C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%//AB029034

C-NT2RP2000027

C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60)//3.30E-16//114aa//44%//002675

C-NT2RP2000198

C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1)//6.00E-16//124aa//34%//P41238

C-NT2RP2000551

C-NT2RP2000644

C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

C-NT2RP2000678

C-NT2RP2000715

C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811

C-NT2RP2000970

C-NT2RP2001347

C-NT2RP2001460//TRICHOHYALIN//1.00E-14//521aa//24%//P37709

C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNITD.//6.10E-12//184aa//31%//P24391

C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067

C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//0//1287bp//99%//AF058718

C-NT2RP2001677

C-NT2RP2001678

C-NT2RP2001720

C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1)//7.90E-52//220aa//44%//Q61068

C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//1.70E-49//411aa//32%//P51523

C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009

C-NT2RP2001861

C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//014754

C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1)//1.20E-45//141aa//65%//P55008

C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161

C-NT2RP2001936

C-NT2RP2001943

C-NT2RP2001946

C-NT2RP2002032

C-NT2RP2002033

C-NT2RP2002034

C-NT2RP2002044

C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5Hz mRNA, complete cds.//1.60E-226//1301bp//88%//U87306

C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1772bp//95%//AB029020  
 C-NT2RP2002172  
 C-NT2RP2002219  
 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418  
 5 C-NT2RP2002316  
 C-NT2RP2002373  
 C-NT2RP2002439  
 C-NT2RP2002475  
 C-NT2RP2002546  
 10 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523  
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181  
 C-NT2RP2002643  
 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107  
 15 C-NT2RP2002736  
 C-NT2RP2002740  
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016  
 C-NT2RP2002752  
 C-NT2RP2002753  
 20 C-NT2RP2002857  
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.90E-11//132aa//38%//Q13829  
 C-NT2RP2003073  
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545  
 25 C-NT2RP2003206  
 C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//0//2870bp//98%//X74794  
 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657  
 C-NT2RP2003237  
 30 C-NT2RP2003272//Homo sapiens ubiquitin mRNA, complete cds.//0//1789bp//99%//AF176069  
 C-NT2RP2003280  
 C-NT2RP2003293  
 C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//P25386  
 35 C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//061068  
 C-NT2RP2003456  
 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783  
 40 C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158  
 C-NT2RP2003559  
 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//2.10E-59//270aa//46%//P19474  
 45 C-NT2RP2003581  
 C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215  
 C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%//AF098786  
 50 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637  
 C-NT2RP2003727  
 C-NT2RP2003751  
 C-NT2RP2003820  
 C-NT2RP2003871

C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//0//2866bp//98%//AB007916

C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)//  
2.30E-53//141aa//78%/P20290

C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) //5.40E-30//319aa//31%//Q01513

C-NT2RP2004142

C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781

C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds./3.80E-52/397bp/82%/AF003998

C-NT2RP2004207

C-NT2RP2004226

C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//AB015982

C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//9.90E-12//427aa//26%//P19246

C-NT2RP2004270//PROTEIN PTM1 PRECURSOR//1.40E-16//334aa//24%//P32857

C-NT2RP2004321

C-NT2RP2004339

C-NT2RP2004347

C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//99%//AB028069

C-NT2RP2004399

C-NT2RP2004400

C-NT2RP2004412

C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds //0//2321bp//86%//AF155739

C-NT2RP2004490

C-NT2RP2004523

C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//AF090190

C-NT2RP2004580

C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds.//0//2886bp//100%//AB020695

C-NT2RP2004594

C-NT2RP2004681

C-NT2RP2004709

C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds.//0//2587bp//100%//AB023231

C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//0//1774bp//99%//AB020691

C-NT2RP2004767

C-NT2RP2004775

C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-228//1666bp//75%//U56732

C-NT2RP2004962

C-NT2RP2004982

C-NT2RP2005003//52 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//  
1.80E-99//376aa//43%/P19474

C-NT2RP2005018

C-NT2RP2005020

C-NT2RP2005022

C-NT2RP2005031

C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds./0//4069bp/99%//AB014564

C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.4) (2-5A-DEPENDENT RNAASE)

RIBONUCLEASE A: 1.0 mg/ml

DOI:10.1002/for

NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//

99%//AF124735

C-NT2RP2005336//TRICHOHYALIN//5.40E-10//545aa//22%//P37709

C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38)//2.10E-124//636aa//38%//P32660

5 C-NT2RP2005360

C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN//5.30E-63//410aa//40%//P22059

C-NT2RP2005454

C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-130//608bp//99%//AF070652

10 C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032

C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B)//0.00000015//279aa//26%//P35418

C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742

C-NT2RP2005501

C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1)//5.50E-70//393aa//39%//P11171

15 C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0//2554bp//99%//AB028943

C-NT2RP2005645

C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR//2.60E-10//175aa//27%//Q92834

C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN)//3.00E-63//323aa//39%//Q62158

20 C-NT2RP2005741

C-NT2RP2005806

C-NT2RP2005815

C-NT2RP2005841

C-NT2RP2005882

25 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//1.50E-67//388aa//44%//P25500

C-NT2RP2006103

C-NT2RP2006166

C-NT2RP2006258

30 C-NT2RP2006261

C-NT2RP2006321

C-NT2RP2006454

C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538

35 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR//4.60E-78//421aa//37%//P32559

C-NT2RP3000047//NPL4 PROTEIN//1.10E-85//526aa//36%//P33755

C-NT2RP3000418

C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION//2.90E-1511319aa//26%//P37908

40 C-NT2RP3000487

C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus//0//1934bp//99%//X16667

C-NT2RP3000526

C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1//3.70E-11//90aa//42%//Q13562

C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265

45 C-NT2RP3000628

C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)//1.40E-24//155aa//37%//Q10149

C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.)//8.30E-108//331aa//50%//P27448

50 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.90E-46//73aa//98%//P39027

C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//9.00E-201//584aa//54%//Q05481

C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//2.90E-11//631aa//23%//P25386

55 C-NT2RP3001113

C-NT2RP3001113

C-NT2RP3001113

C-NT2RP3001113

C-NT2RP3001383

C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538

C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1]//1.40E-76//388aa//32%//P46821

5 C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534

C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177

C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554

10 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141

C-NT2RP3001739

C-NT2RP3001777

C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808

C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//0//3747bp//99%//AB014575

15 C-NT2RP3001944

C-NT2RP3002033

C-NT2RP3002054

C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds.//0//2830bp//99%//AB028956

C-NT2RP3002099

20 C-NT2RP3002102

C-NT2RP3002147

C-NT2RP3002163

C-NT2RP3002173

C-NT2RP3002255

25 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE)//8.60E-49//243aa//43%//Q58767

C-NT2RP3002343

C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396

30 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)(P1-CDC21).//8.60E-79//416aa//34%//P33991

C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//0//3811bp//99%//AB014578

C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//99%//AL050092

35 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010

C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598

C-NT2RP3002603

40 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660

C-NT2RP3002659

C-NT2RP3002660

C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903

45 C-NT2RP3002687

C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kifib), complete cds.//1.10E-93//1205bp//69%//D17577

C-NT2RP3002701

C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371

C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430

50 C-NT2RP3002876

C-NT2RP3002877

C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0//2085bp//94%//AB018314

C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053

C-NT2RP3002972//Halocynthia roretzi mRNA for HRPET-1, complete cds.//3.90E-52//899bp//61%//AB111111

C-NT2RP3003061//ANKYRIN //1.40E-20//200aa//37%//Q02357

C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645

- C-NT2RP3003078  
C-NT2RP3003139  
C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//AF07773 8
- 5 C-NT2RP3003150  
C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa//31%//Q09674  
C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851bp//76%//AF110267
- 10 C-NT2RP3003210  
C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286  
C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656  
C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//AF098462
- 15 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A))//4.20E-86//366aa//48%//P19474  
C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)//1.10E-170//585aa//54%//064948
- 20 C-NT2RP3003311  
C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653  
C-NT2RP3003427  
C-NT2RP3003543
- 25 C-NT2RP3003552  
C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%//P40529  
C-NT2RP3003564  
C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//AF106681
- 30 C-NT2RP3003621  
C-NT2RP3003625  
C-NT2RP3003656  
C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- 35 C-NT2RP3003686  
C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446  
C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014  
C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//U28164
- 40 C-NT2RP3003795  
C-NT2RP3003805  
C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590  
C-NT2RP3003819  
C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
- 45 C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523  
C-NT2RP3003833  
C-NT2RP3003842
- 50 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//AB019435  
C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%//AB018343  
C-NT2RP3003876  
C-NT2RP3003914//UDP-GLUCOSE GLYCOPROTEIN GLUCOSYL TRANSFERASE (UGT1A1) mRNA, complete cds.//0//2557bp//99%//AB018343
- C-NT2RP3003915//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%//AB018343  
AF086628  
C-NT2RP3003989

C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1)  
 (KRAB-ASSOCIATED PROTEIN 1)//1.50E-17//226aa//26%//Q13263  
 C-NT2RP3004070  
 C-NT2RP3004145  
 5 C-NT2RP3004215  
 C-NT2RP3004253  
 C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871  
 C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//  
 X67877  
 10 C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0//1778bp//99%//AC003982  
 C-NT2RP3004503  
 C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//1.20E-95//434aa//43%//  
 P51523  
 15 C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST),  
 complete cds.//0//2393bp//99%//AB014679  
 C-NT2RP4000023  
 C-NT2RP4000218  
 C-NT2RP4000424  
 C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT)//5.70E-141//511aa//43%//Q99676  
 20 C-NT2RP4001447  
 C-NT2RP4001841  
 C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194  
 C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//067618  
 C-NT2RP4002075  
 25 C-NT2RP4002083  
 C-OVARC1000001/Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//  
 99%//AB029290  
 C-OVARC1000008  
 C-OVARC1000017  
 30 C-OVARC1000058  
 C-OVARC1000068  
 C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//  
 727bp//67%//AF156957  
 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761  
 35 C-OVARC1000109  
 C-OVARC1000114  
 C-OVARC1000145  
 C-OVARC1000240  
 C-OVARC1000302  
 40 C-OVARC1000408  
 C-OVARC1000414  
 C-OVARC1000440  
 C-OVARC1000442  
 C-OVARC1000496  
 45 C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2)  
 (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3)//3.30E-67//132aa//95%//015349  
 C-OVARC1000557  
 C-OVARC1000578  
 C-OVARC1000622  
 50 C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888  
 C-OVARC1000681  
 C-OVARC1000700  
 C-OVARC1000724  
 C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C (P23511) (EC 3.1.3.42) (PP2C-  
 711a//37%//P43554  
 C-OVARC1000855//OXIDOREDUCTASE UCPA (EC 1.1.1.-)//1.30E-32//170aa//34%//P37440

C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37)//0.0000054//135aa//28%//P03398  
 C-OVARC1000937//S-PHASE ENTRY CYCLIN 6//4.90E-10//61aaa//49%//P32943  
 C-OVARC1000960  
 C-OVARC1000971  
 5 C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR//4.10E-11//189aa//32%//Q06527  
 C-OVARC1001000  
 C-OVARC1001029  
 C-OVARC1001040  
 10 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
 EPS15) (AF-1P PROTEIN)//1.10E-08//216aa//23%//P42566  
 C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//5.1e-310//1588bp//93%//  
 AF051782  
 C-OVARC1001118  
 C-OVARC1001129  
 15 C-OVARC1001169  
 C-OVARC1001240  
 C-OVARC1001261  
 C-OVARC1001339  
 20 C-OVARC1001342//40S RIBOSOMAL PROTEIN S8//1.40E-110//207aa//99%//P09058  
 C-OVARC1001357  
 C-OVARC1001442  
 C-OVARC1001611  
 C-OVARC1001813  
 25 C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//0//1760bp//99%//AF054174  
 C-OVARC1002143  
 C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-  
 REDUCTASE 2) (SR TYPE 2)//7.60E-08//114aa//37%//P31213  
 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP)//1.70E-  
 09//207aa//30%//Q91854  
 30 C-PLACE1000014  
 C-PLACE1000078  
 C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds//0//2041bp//87%//  
 U35245  
 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN//1.70E-07//251aa//24%//P23645  
 35 C-PLACE1000814  
 C-PLACE1000979//ZINC FINGER PROTEIN 135//2.50E-153//326aa//64%//P52742  
 C-PLACE1001007  
 C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds//4.00E-300//  
 1355bp//100%//AB024301  
 40 C-PLACE1001088  
 C-PLACE1001136  
 C-PLACE1001241  
 C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//5.90E-228//827bp//99%//  
 AF009615  
 45 C-PLACE1001395  
 C-PLACE1001740  
 C-PLACE1001746  
 C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION//7.50E-16//  
 319aa//26%//P37908  
 50 C-PLACE1002066  
 C-PLACE1002115  
 C-PLACE1002213  
 C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//0//1657bp//98%//AB018271  
 C-PLACE1002450//Human zinc finger protein mRNA, complete cds//0//2565bp//99%//U69274  
 55 C-PLACE1002474//M...  
 C-PLACE1002571  
 C-PLACE1002714

C-PLACE1002772

C-PLACE1002775//PEREGRIN (BR140 PROTEIN)//3.80E-13//272aa//28%/P55201

C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//5.50E-203//396aa//86%/P51522

5 C-PLACE1002993

C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//8.50E-44//225bp//100%/AF032387

C-PLACE1003205

C-PLACE1003249

10 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSORS//1.70E-23//594aa//33%/P28481

C-PLACE1003553

C-PLACE1003592

C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG//2.60E-93//270aa//66%/P46975

15 C-PLACE1003669//TRICHOHYALIN//5.60E-09//219aa//30%/P22793

C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds//6.20E-282//1316bp//98%/AF053305

C-PLACE1003870

20 C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//3.70E-222//651aa//66%/P25500

C-PLACE1003892

C-PLACE1003900

C-PLACE1004336

C-PLACE1004384

25 C-PLACE1004425

C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//2.90E-56//276aa//41%/P51522

C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds//2.10E-16//402bp//62%/U90878

30 C-PLACE1004518

C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds//3.50E-274//1305bp//97%/AF132954

C-PLACE1004681

C-PLACE1004693

C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds//2.70E-103//586bp//91%/AF125099

35 C-PLACE1004815

C-PLACE1004836

C-PLACE1004838

C-PLACE1004840

C-PLACE1004900

40 C-PLACE1004985

C-PLACE1005085

C-PLACE1005086

C-PLACE1005108

C-PLACE1005146

45 C-PLACE1005409

C-PLACE1005453

C-PLACE1005477

C-PLACE1005557//60S RIBOSOMAL PROTEIN L27//1.90E-11//60aa//48%/P46288

C-PLACE1005595

50 C-PLACE1005603

C-PLACE1005639

C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds//2.00E-118//378bp//98%/AF162680

C-PLACE1005799

C-PLACE1005800

C-PLACE1005801

C-PLACE1005968

C-PLACE1006002

C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852

C-PLACE1006017

C-PLACE1006037

C-PLACE1006076

5 C-PLACE1006143

C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//1489bp//100%//AB014548

C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//4.60E-117//147aa//80%//P21796

10 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374

C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//1.30E-18//460aa//24%//Q00547

C-PLACE1006371

15 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.20E-83//313aa//49%//P27550

C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//2170bp//99%//AF191338

C-PLACE1006521

20 C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//883bp//99%//AL110144

C-PLACE1006617

C-PLACE1006640

C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//6.20E-63//191aa//43%//P13688

25 C-PLACE1006760

C-PLACE1006779

C-PLACE1006805

C-PLACE1006815

C-PLACE1006867

30 C-PLACE1007045

C-PLACE1007097

C-PLACE1007111

C-PLACE1007112

C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%//AB023226

35 C-PLACE1007218

C-PLACE1007454

C-PLACE1007478

C-PLACE1007677

40 C-PLACE10077057//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%//AB033922

C-PLACE1007737

C-PLACE1007743

C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%//AB020685

45 C-PLACE1007877

C-PLACE1008045

C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179

C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.)//3.00E-25//208aa//37%//Q03326

C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077

50 C-PLACE1008231

C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808

C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN- 10).//2.20E-23//94aa//47%//Q05315

C-PLACE1008331

C-PLACE1008331

C-PLACE1008331

C-PLACE1008400

C-PLACE1008424

C-PLACE1008584

C-PLACE1008625

C-PLACE1008630

C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)//5.20E-90//483aa//38%//002668

C-PLACE1008715

C-PLACE1008748

C-PLACE1008757

C-PLACE1008798

C-PLACE1008851

C-PLACE1008947

C-PLACE1009039

C-PLACE1009048

C-PLACE1009050

C-PLACE10091137//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//0//2529bp//99%//AF035586

C-PLACE1009150

C-PLACE1009200

C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3//4.40E-16//82aa//43%//P29675

C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds//0//2262bp//99%//AF191298

C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN//4.00E-06//439aa//23%//P14922

C-PLACE1009398//ZINC FINGER PROTEIN 135//6.20E-97//361aa//51%//P52742

C-PLACE1009410

C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds//6.50E-148//592bp//99%//AB014584

C-PLACE1009493

C-PLACE1009539

C-PLACE1009595

C-PLACE1009637

C-PLACE1009639

C-PLACE1009798//RLR1 PROTEIN//1.60E-18//270aa//23%//P35552

C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-)//6.50E-28//209aa//38%//P43510

C-PLACE1009888

C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds//0//1730bp//99%//AF038963

C-PLACE1009947

C-PLACE1010069

C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds//0//1554bp//100%//AB029020

C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)//5.10E-27//371aa//28%//Q14246

C-PLACE1010270

C-PLACE1010562

C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, complete cds//9.30E-299//1362bp//99%//AF200715

C-PLACE1010624

C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds//7.50E-08//324bp//64%//AF109907

C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT)//1.80E-222//808aa//52%//Q09332

C-PLAC.E1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//5.20E-151//427aa//55%//P28160

C-PLACE1010761

C-PLACE1010802 C-PLACE1010833//CALTRACTIN (CENTRIN)//0.0000001//154aa//28%//P41209

C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//1.50E-25//583aa//23%//P35580

C-PLACE1010896

C-PLACE1010896

C-PLACE1010896

C-PLACE1011032

C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019  
 C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256  
 C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//99%//AL050159  
 5 C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663  
 C-PLACE1011214  
 C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604  
 C-PLACE1011273  
 10 C-PLACE1011291  
 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587  
 C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703  
 C-PLACE1011503  
 15 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377  
 C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752  
 C-PLACE1011650  
 C-PLACE1011675  
 20 C-PLACE1011725  
 C-PLACE1011749  
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580  
 C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256  
 25 C-PLACE2000006  
 C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0//1968bp//97%//AB020720  
 C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%//P10586  
 C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//4.60E-291//1167bp//89%//L08505  
 30 C-PLACE2000061  
 C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219  
 C-PLACE2000097  
 C-PLACE2000103  
 35 C-PLACE2000115  
 C-PLACE2000124  
 C-PLACE2000140  
 C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736  
 C-PLACE2000176  
 40 C-PLACE2000223  
 C-PLACE2000235  
 C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098  
 C-PLACE2000302  
 C-PLACE2000347  
 45 C-PLACE2000359  
 C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205  
 C-PLACE2000379  
 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209  
 50 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996  
 C-PLACE2000450  
 C-PLACE2000455  
 C-PLACE3000059//Mus musculus mRNA for ubiquitin-conjugating enzyme.//0//1670bp//99%//U00000  
 C-PLACE3000067  
 C-PLACE3000112//Homo sapiens mRNA for ubiquitin-conjugating enzyme.//0//1670bp//99%//U00000  
 C-PLACE3000136

C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084

C-PLACE3000148

C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.10E-75//382bp//99%//AB014572

C-PLACE3000160

C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742

C-PLACE3000194

C-PLACE3000199

C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020

C-PLACE3000230

C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995

C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946

C-PLACE3000276

C-PLACE3000310

C-PLACE3000320

C-PLACE3000331

C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23 %//P08640

C-PLACE3000352

C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp586H0623).//0//2456bp//99%//AL096739

C-PLACE3000362

C-PLACE3000365

C-PLACE3000388

C-PLACE3000413

C-PLACE3000425

C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580

C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100

C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281

C-PLACE4000089

C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aa//88%//AF091234

C-PLACE4000129

C-PLACE4000147

C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746

C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//1.70E-262//1217bp//98%//AF000422

C-PLACE4000222

C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3787bp//99%//AB028990

C-PLACE4000270

C-PLACE4000300

C-PLACE4000387

C-PLACE4000392

C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200

C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//2.70E-261//1217b.p//98%//AF000422

C-PLACE4000465

C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELE-1) (ELEMENT-BINDING ACTIVITY) (TRANSCRIPTION FACTOR).//0//1000bp//99%//AF000422

C-PLACE4000500//Mus musculus mRNA for Karyopherin beta-4 subunit, putative enzyme.//5.50E-35//431aa//29%//O60100

C-PLACE4000500//Mus musculus mRNA for Karyopherin beta-4 subunit, putative enzyme.//5.50E-35//431aa//29%//O60100

C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800  
 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655  
 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709

5 C-THYRO1000070

C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799

C-THYRO1000092

C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%//AB029039

10 C-THYRO1000124

C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698

C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%//AB014552

C-THYRO1000206

C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//P51523

15 C-THYRO1000253

C-THYRO1000270

C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068

C-THYRO1000320

20 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563

C-THYRO1000368

C-THYRO1000381

C-THYRO1000387

C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%//AF072864

C-THYRO10003957//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857

C-THYRO1000401

C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663

C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-98//408aa//42%//P19474

30 C-THYRO1000558

C-THYRO1000570

C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360

35 C-THYRO1000625

C-THYRO1000637

C-THYRO1000676

C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679

C-THYRO1000712

40 C-THYRO1000805

C-THYRO1000815

C-THYRO1000855

C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%//P32322

45 C-THYRO1000988

C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948

C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//1479bp//66%//U38252

C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276

50 C-THYRO1001262

C-THYRO1001271

C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701

C-THYRO1001312

C-THYRO1001334

C-THYRO1001363//Homo sapiens mRNA cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp//98%//AL080120

C-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//0//1700bp//99%//AB014607

C-THYRO1001403

C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427

C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%//AF078850

C-THYRO1001426

C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580

C-THYRO1001480

C-THYRO1001487

C-THYRO1001584

C-THYRO1001661

C-THYRO1001746

C-THYRO1001772

C-THYRO1001854

C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81 %//AF171060

C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484

C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%//AF123534

C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835

C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692

C-Y79AA1000410

C-Y79AA1000539

C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.00E-302//1375bp//99%//AF091080

C-Y79AA1000802

C-Y79AA1000827

C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757

C-Y79AA1000969

C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962

C-Y79AA1001061

C-Y79AA1001068

C-Y79AA1001216

C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738

C-Y79AA1001511

C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%//Q00547

C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//1.40E-78//227aa//40%//Q01820

C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//AF192913

C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489

C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133

C-Y79AA1002210//YTUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.0000018//140aa//25%//Q13829

C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//146aa//35%//016264

C-Y79AA1002220

C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//0//3168bp//99%//AB014592

C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384

C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//Y18208

C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725

C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//2.70E-137//340aa//51%/Q05481

C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-310//1444bp//98%/AF129534

C-HEMBA1000290

C-HEMBA1000459

C-HEMBA1000505

C-HEMBA1001196//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%/J04088

C-HEMBA1002503

C-HEMBA1002508

C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%/AJ011972

C-HEMBA1003480

C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41)//2.40E-110//242aa//58%/P00736

C-HEMBA10036451//TTPD PROTEIN.//2.40E-10//289aa//23%/O15736

C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%/AB023230

C-HEMBA1003667

C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%/P23253

C-HEMBA1003827

C-HEMBA1003838

C-HEMBA1004055

C-HEMBA1004056

C-HEMBA1004086

C-HEMBA1004335

C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%/Q99471

C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%/Q61221

C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%/AF201333

C-HEMBA1004507

C-HEMBA1004638

C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%/P18583

C-HEMBA1004709

C-HEMBA1004860

C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%/AJ250308

C-HEMBA1005472

C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%/002193

C-HEMBA1005572

C-HEMBA1005780

C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%/AF082516

C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%/Q61001

C-HEMBA1006124

C-HEMBA1006461

C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%/P25716

C-HEMBA1006617

C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%/O15509

C-HEMBA1006779

C-HEMBA1006796

C-HEMBA1006812

C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//183bp//100%/AF082516

C-HEMBA1007000//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%/AB023230

C-HEMBA1007000

C-HEMBA1007000//CHL1 PROTEIN.//9.50E-19//104aa//45%/P22516

C-HEMBB1000335  
 C-HEMBB1000337  
 C-HEMBB1000554  
 C-HEMBB1000573  
 5 C-HEMBB1000749  
 C-HEMBB1000774  
 C-HEMBB1000835  
 C-HEMBB1001197  
 C-HEMBB1001315  
 10 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001500  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001619  
 15 C-HEMBB1001630  
 C-HEMBB1001665  
 C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%//AB029031  
 C-HEMBB1001812  
 C-HEMBB1001834  
 20 C-HEMBB1001869  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S 1).//5.40E-75//  
 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 25 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 30 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001925  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002152  
 35 C-HEMBB1002300  
 C-HEMBB1002381  
 C-HEMBB1002383  
 C-HEMBB1002534  
 C-MAMMA1000143  
 40 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//  
 P51523  
 C-MAMMA1000227  
 C-MAMMA1000257  
 C-MAMMA1000264  
 45 C-MAMMA1000270  
 C-MAMMA1000279  
 C-MAMMA1000372  
 C-MAMMA1000559  
 C-MAMMA1000752  
 50 C-MAMMA1000760  
 C-MAMMA1000778  
 C-MAMMA1000855  
 C-MAMMA1000859  
 C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN 1 (SERPINF1) (SERPINF1)  
 SERPINF1  
 C-MAMMA1000944  
 C-MAMMA1001070  
 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6E-312//1596bp//94%//

AF067420

C-MAMMA10011987/Homo sapiens eps15RmRNA, partial cds.//0//2253bp//99%//AB015346

C-MAMMA1001202

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978

5 C-MAMMA1001252

C-MAMMA1001296

C-MAMMA1001502

C-MAMMA1001630

C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910

10 C-MAMMA1001683

C-MAMMA1001715

C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687

C-MAMMA1001760

15 C-MAMMA1001769

C-MAMMA1001785

C-MAMMA1001848

C-MAMMA1001874

C-MAMMA1001956

20 C-MAMMA1002009

C-MAMMA1002033

C-MAMMA1002155

C-MAMMA1002498

C-MAMMA1002545

25 C-MAMMA1002571

C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3)(GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640

C-MAMMA1002590

C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742

30 C-MAMMA1002618

C-MAMMA1002636

C-MAMMA1002646

C-MAMMA1002665

C-MAMMA1002708

35 C-MAMMA1002728

C-MAMMA1002744

C-MAMMA1002764

C-MAMMA1002765

C-MAMMA1002830

40 C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178

C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590

C-MAMMA1002880

C-MAMMA1002892

45 C-MAMMA1002909

C-MAMMA1002941

C-MAMMA1002947

C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343

50 C-MAMMA1002973

C-MAMMA1002987

C-MAMMA1003003

C-MAMMA1003026//Homo sapiens HSPC057 mRNA, complete cds.//0//1773bp//98%//AF161542

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-MAMMA1003031

C-NT2RM1000341

C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097

C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731

5 C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775

C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-)//5.60E-08//187aa//27%[/P49695](#)

C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458

10 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//  
AF082516

C-NT2RM1001082

C-NT2RM1001112

C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//AF053091

15 C-NT2RM2001360//Homo sapiens clone C40 unknown mRNA.//1.00E-250//1136bp//100%//AF103798

C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds./0//2300bp//100%/AL110217

C-NT2RM2001803//Homo sapiens IkappaB kinase cbmplex associated protein (IKAP) mRNA, complete cds.//0//  
2249bp//99%//AF044195

20 C-NT2RM4002504

C-NT2RP1000409

C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds.//0//3199bp//99%//AB028991

C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//99%//AF173378

25 C-NT2RP1000796

C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522

C-NT2RP2001214

C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481

C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds./0//3712bp//99%//AB024334

C-NT2RP2002056

C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634

35 C-NT2RP2002333

C-NT2RP2002677

C-NT2RP2002755

C-NT2RP2002843

C-NT2RP2003101

40 C-NT2RP2003668

C-NT2RP2003799

C-NT2RP2004095

C-NT2RP2004300

C-NT2RP2004675

45 C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-  
CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//  
22%/Q61687

C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.10E-308//1437bp//98%//AF045583

50 C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444

C-NT2RP2005726

C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-TRANSFERASE).//4.40E-55//358aa//42%/P51005

C-NT2RP2005980

• 2RDC006-24

REF ID: A66534

MA CHAIN FRAGMENT: 32L 11/32aa/96%/Q1313'

C-NT2RP2006554

C-NT2RP3000584

C-NT2RP3001115

C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds//1.40E-58//1138bp//63%//AF193613

5 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-)//1.30E-22//227aa//33%//P08458

C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds//0//2443bp//99%//U87791

C-NT2RP3002402

C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds//1.20E-124//597bp//98%//AB023215

C-NT2RP3002512

10 C-NT2RP3002713

C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116//1.00E-07//70aa//41%//P17564

C-NT2RP3002799

C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4//2.20E-10//260aa//26%//Q31125

15 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN//5.70E-226//303aa//97%//P51026

C-NT2RP3002955

C-NT2RP3002985

20 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds//3.80E-152//1007bp//82%//U78090

C-NT2RP3003121

C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds//0//1998bp//91%//AB011414

25 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds//0//2159bp//98%//AF071592

C-NT2RP3003155

C-NT2RP3003157

C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33//2.80E-06//402aa//23%//P49455

C-NT2RP3003264

30 C-NT2RP3003346

C-NT2RP3003403

C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds//6.30E-270//743bp//90%//AF071317

C-NT2RP3003500//SCY1 PROTEIN//9.20E-27//601aa//23%//P53009

35 C-NT2RP3003572

C-NT2RP3003576

C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds//0//1690bp//99%//AB013885

C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7)//2.20E-13//146aa//42%//P14209

40 C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds//0//2047bp//95%//AL080155

C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds//9.00E-238//1529bp//84%//U71294

C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds//1.90E-163//924bp//89%//AF130457

45 C-NT2RP3003828

C-NT2RP3003932

C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186)//0//2739bp//99%//AL050019

C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein//6.50E-240//1215bp//94%//X84692

50 C-NT2RP3004028

C-NT2RP3004041

C-NT2RP3004051

C-NT2RP3004078//H.sapiens HRFX2 mRNA//0//1806bp//99%//X76091

C-NT2RP3004093

C-NT2RP3004125

C-NT2RP3004125//Mus musculus mRNA for RNA binding protein//6.50E-240//1215bp//94%//X84692

C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-

DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //7.90E-05//271aa//22%//P08640

C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948

C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.30E-14//242aa//24%//Q00808

C-NT2RP3004332

5 C-NT2RP3004349

C-NT2RP3004470

C-NT2RP4000035

C-NT2RP4000049

C-NT2RP4000102

10 C-NT2RP4000167

C-NT2RP4000515

C-NT2RP4000517

C-NT2RP4000519

C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%//AB033117

15 C-OVARC1000092

C-OVARC1000533

C-OVARC1000678

C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//0//2032bp//99%//AL133014

20 C-OVARC1000802

C-OVARC1000890

C-OVARC1000891

C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//82%//AB005549

25 C-OVARC1001072

C-OVARC1001117

C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192

C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//X62083

30 C-OVARC1001329

C-OVARC1001341

C-OVARC1001376

C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//AF016507

35 C-OVARC1001873

C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) //1.60E-81//212aa//70%//P34547

40 C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421

C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%//AB023234

C-PLACE1001076

C-PLACE1001118//ZINC FINGER PROTEIN 135//5.40E-147//443aa//57%//P52742

C-PLACE1001366

45 C-PLACE1001545

C-PLACE1001608

C-PLACE1002004

C-PLACE1002256

C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233

50 C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%//P31146

C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765

C-PLACE1003383

C-PLACE1003864

C-PLACE1004491

C-PLACE1004979

C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950

C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%//AB011148

C-PLACE1005128

C-PLACE1005162

C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%//AF113539

C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A)//1.10E-09//93aa//31%//P32959

C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%//AJ010046

C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6)//6.80E-09//267aa//30%//P29128

C-PLACE1005611//Mus musculus mRNA for mDjIO, complete cds.//2.00E-33//379bp//66%//AB028860

C-PLACE1005802

C-PLACE1005850

C-PLACE1005898

C-PLACE1005932

C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%//AF161542

C-PLACE1006360

C-PLACE1006795

C-PLACE1006878//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-NUCLEASE)//1.90E-08//122aa//36%//P16658

C-PLACE1007557

C-PLACE1007807

C-PLACE1008181

C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%//AB033114

C-PLACE1008455

C-PLACE1008941

C-PLACE1009935

C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//1.20E-18//467aa//30%//P46804

C-PLACE1011891

C-PLACE10118967//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969

C-PLACE2000003

C-PLACE2000132

C-PLACE2000170

C-PLACE2000335

C-PLACE3000124

C-PLACE3000158

C-PLACE3000207

C-PLACE3000221

C-PLACE3000271

C-PLACE3000304

C-PLACE3000322

C-PLACE3000341

C-PLACE3000373

C-PLACE3000399

C-PLACE3000401

C-PLACE3000402

C-PLACE3000406

C-PLACE3000475

C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//1.70E-15//740aa//23%//P08640

C-PLACE4000093

C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//AF146689

C-PLACE4000131//Homo sapiens mRNA, cDNA DKFZp586J0217 (from clone DKFZp586J0217)

C-PLACE400024

C-PLACE4000250

C-PLACE4000252

C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200  
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201  
 C-PLACE4000320  
 C-PLACE4000344  
 5 C-PLACE4000367  
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME).//7.20E-22//54aa//62%//Q01576  
 C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.//  
 0//2159bp//98%//AL117654  
 10 C-PLACE4000487  
 C-PLACE4000494  
 C-PLACE4000521  
 C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%//AB023164  
 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mito-  
 15 chondrial protein, complete cds.//0//2384bp//99%//AF047690  
 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//  
 AB021663  
 C-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%//AB018333  
 C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//  
 20 AF118566  
 C-THYRO1001142  
 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (H1PF7).//1.10E-200//546aa//  
 62%//005481  
 C-THYRO1001320  
 25 C-THYRO1001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.//  
 0//1010bp//98%//AL050159  
 C-THYRO1001602  
 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652  
 C-THYRO1001828  
 30 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//  
 AF157833  
 C-Y79AA1001167  
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//  
 4708bp//99%//AF055084  
 35 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415  
 C-HEMBA1006092  
 C-HEMBA1006406  
 C-HEMBB1000790  
 40 C-HEMBB1000917  
 C-HEMBB1002280  
 C-MAMMA1000802  
 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//  
 P20931  
 45 C-MAMMA1002597  
 C-MAMMA1002868  
 C-NT2RP2003161  
 C-NT2RP2003339  
 C-NT2RP3001282  
 50 C-PLACE1001761  
 C-PLACE1004491  
 C-PLACE1004686  
 C-PLACE1005574  
 C-PLACE1006382  
 C-PLACE3000451  
 C-PLACE4000230//Mus musculus semaphorin v.1 mRNA, complete cds.//0//2567bp//88%//AF030430  
 C-THYRO1000916

C-HEMBA1000327  
 C-HEMBA1000637  
 C-HEMBA1001967  
 C-MAMMA1000266  
 5 C-NT2RP2002979  
 C-PLACE1007866  
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK)  
 (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa//45%/Q13177  
 C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-151//476aa//46%/P52740  
 10 C-THYRO1001637  
 C-MAMMA1002215  
 C-MAMMA1002721  
 C-NT2RP2002070

15 Homology search result 14.

**[0334]** Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.90E-250//554aa//85%/061712  
 C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)  
 25 (LEURS).//6.40E-99//457aa//45%/Q09996  
 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.50E-264//1194bp//95%/X02344  
 C-HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.//0//1759bp//99%/AF124490  
 C-HEMBA1000129//HYPOTHETICAL HEUCASE C8A4.08C IN CHROMOSOME 1.//3.80E-25//166aa//36%/Q09884  
 30 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%/AF196304  
 C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds.//5.20E-213//525bp//99%/AF085356  
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.90E-12//368aa//24%/P08553  
 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5.00E-16//166aa//36%/P35584  
 C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE D.//2.90E-14//303aa//25%/P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.40E-12//125aa//31%/P48555  
 40 C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%/AJ011738  
 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.00E-86//146aa//56%/Q61221  
 C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.10E-254//1440bp//87%/AF030131  
 45 C-HEMBA1000304//Rattus norvegicus Ca<sup>2+</sup>-dependent activator protein (CAPS) mRNA, complete cds.//5.10E-131//712bp//91%/U16802  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-49//107aa//91%/035594  
 C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%/AF174601  
 50 C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds.//0//1949bp//98%/AB026491  
 C-HEMBA1000411//ANKYRIN.//5.70E-12//127aa//38%/Q02357  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.30E-45//481aa//29%/Q04652  
 C-HEMBA1000491//RAS LIKE PROTEIN 2.//2.00E-22//188aa//31%/P22275  
 C-HEMBA1000523//TESTIS-ABUNDANT PROTEIN, PRS1.//4.0E-44//282aa//31%/P22275  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.60E-12//73aa//41%/P02826

- C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.20E-194//663bp//83%//D89340
- C-HEMBA1000555//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//7.90E-226//1501bp//83%//AF156529
- 5 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//25 %//Q05481
- C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aabb//32%//Q60865
- C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.10E-144//602bp//77%//AF045573
- 10 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246
- C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.//0//1465bp//99%//AF121856
- C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.80E-55//179aa//61%//O43295
- C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.20E-156//1366bp//76%//U35776
- 15 C-HEMBA1000851//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1862bp//99%//AF173868
- C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1.00E-78//119aa//87%//P51689
- C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.60E-30//127aa//40%//P43366
- 20 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1.00E-10//288aa//23%//Q19124
- C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493
- C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.40E-12//131aa//38%//Q01485
- 25 C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//99%//U06088
- C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%//P02461
- C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%//AF119043
- 30 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50//176aa//57%//P48059
- C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065)(HA0946) (FRAGMENT).//1.50E-116//197aa//58%//Q06730
- 35 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%//P51646
- C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%//AF112221
- C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
- C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401
- 40 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp//94%//AF153686
- C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.40E-133//614bp//99%//AF057358
- C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%//P17081
- 45 C-HEMBA1001405//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//5.60E-25//863bp//60%//AF053091
- C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%//AF112221
- C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%//AF205599
- 50 C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088
- C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%//P18850
- C-HEMBA1001569//SYNAPTOTRIBIN-RELATED PROTEIN ASSOCIATED MEMBRANE PROTEIN (VAMP-1).//3.110aa//100%//P19065
- C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%//AJ012449

C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT)//4.90E-156//348aa//83%//Q14141  
 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS)//1.60E-166//506aa//60%//  
 P42803  
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA)//1.60E-10//155aa//28%//  
 5 Q63679  
 C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCES-  
 SORY PROTEIN 1)//6.20E-07//362aa//24%//Q50365  
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//4.60E-36//  
 365aa//33%//P33450  
 10 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, com-  
 plete cds//0//1707bp//98%//AF072247  
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9//5.40E-09//101aa//35%//  
 P54787  
 C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds//3.70E-78//200bp//  
 15 100%//AB029042  
 C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds//3.10E-267//1212bp//99%//  
 AF195883  
 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OBCADHERIN) (OSF-4)//  
 1.10E-38//87aa//96%//P55288  
 20 C-HEMBA1001744//SCY1 PROTEIN//9.90E-32//481aa//25%//P53009  
 C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, com-  
 plete cds//7.60E-59//998bp//64%//AF098066  
 C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds//0//  
 1637bp//99%//AF125158  
 25 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180//3.80E-11//206aa//36%//P11675  
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT)//2.90E-135//459aa//52%//Q99676  
 C-HEMBA1001822//Mus musculus Ese2L protein mRNA, complete cds//1.90E-235//1329bp//89%//AF132479  
 C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds//1.40E-199//1180bp//89%//  
 AF159025  
 30 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29)//7.60E-64//221aa//55%//Q07230  
 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT)//5.70E-51//234aa//41%//Q09332  
 C-HEMBA1001869//TRITHORAX PROTEIN//9.60E-05//166aa//27%//P20659  
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH)//  
 35 9.30E-36//395aa//26%//Q63342  
 C-HEMBA1001913//GCN20 PROTEIN//2.30E-81//158aa//50%//P43535  
 C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//0//  
 1850bp//99%//AF000145  
 C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds//0//1721bp//99%//AF155114  
 40 C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromodomain adjacent to zinc finger domain 1A, complete  
 cds//0//2149bp//99%//AB032252  
 C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds//1.30E-  
 271//1583bp//88%//U92703  
 C-HEMBA1002102//ANKYRIN//4.40E-10//106aa//35%//Q02357  
 45 C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50)//7.10E-05//51aa//49%//Q14847  
 C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds//1.10E-153//1059bp//82%//AF178669  
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM//1.40E-51//180aa//56%//  
 P79293  
 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4)//6.00E-13//190aa//36%//  
 50 P43694  
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE-2 (EC 2.7.1.112) (FRAGMENT)//3.00E-17//267aa//29%//  
 P18161  
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]//2.20E-199//392aa//89%//P47226  
 C-HEMBA1002241//PROLIFERATING CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION ASSOCIAT  
 ED NUCLEOLAR ANTIGEN)  
 C-HEMBA1002267//Sus scrofa oocyte mRNA, complete cds//0//1302bp//99%//AF125550  
 C-HEMBA1002341//P53-BINDING PROTEIN 2 (53BP2) (FRAGMENT)//3.80E-55//109aa//96%//Q62415  
 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//0//

1847bp//99%//AF092563

C-HEMBA1002417//mGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)//1.00E-121//489aa//52%//P39447

C-HEMBA1002419//TRICHOHYALIN//1.90E-09//299aa//24%//P22793

C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74//4.20E-24//109aa//55%//Q00994

C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT)//3.50E-50//199aa//61%//P98175

C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//1.10E-12//285aa//31%//P17437

C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1//6.80E-53//257aa//36%//P48732

C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//0//2432bp//99%//AJ011972

C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//0//1605bp//97%//AF016903

C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds//5.30E-51//768bp//68%//AF055993

C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//6.80E-305//951bp//99%//AF075587

C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7)//5.00E-37//268aa//34%//P06746

C-HEMBA1002768//Mus musculus formin binding protein 17 mRNA, partial cds//7.80E-237//1522bp//85%//AB011126

C-HEMBA1002770//Rattus norvegicus mRNA for TIP120, complete cds//2.90E-176//1024bp//88%//D87671

C-HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds//3.40E-54//319bp//76%//AF153879

C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//9.2c 314//1437bp//99%//AF071185

C-HEMBA1002818//Homo sapiens mRNA for fibulin-4//2.00E-304//1383bp//99%//AJ132819

C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME n//1.50E-44//188aa//52%//Q09297

C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.30E-15//371aa//25%//Q05481

C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//2.00E-34//300aa//34%//P16157

C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//4.40E-06//324aa//24%//P32380

C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4)//1.20E-27//63aa//100%//P14646

C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//3.80E-25//534aa//24%//Q02224

C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds//1.40E-171//1552bp//75%//U20286

C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA//0//1558bp//99%//AF054182

C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS)//1.30E-09//121aa//40%//P35858

C-HEMBA1003077//SLIT PROTEIN PRECURSOR//2.60E-15//199aa//31%//P24014

C-HEMBA1003096//Mouse 19.5 mRNA, complete cds//5.60E-117//1139bp//72%//M32486

C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds//6.20E-273//1253bp//99%//AF155096

C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)//8.50E-51//221aa//33%//P41940

C-HEMBA1003148//Homo sapiens mRNA for dachshund protein//0//1583bp//99%//AJ005670

C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61)//5.90E-74//134aa//53%//P44551

C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds//8.50E-87//285bp//90%//AF129534

C-HEMBA1003235//TROPOMYOSIN//2.30E-06//109aa//33%//Q02088

C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.1)//7.20E-41//245aa//42%//Q06548

C-HEMBA1003286//Homo sapiens mRNA for protein kinase C delta activity transferase//0//430bp//99%//AB024436

C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10)//7.6.20E-28//126aa//51%//

Q38997

C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.00E-08//248aa//23%/Q02224

C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//7.80E-13//297aa//30%/P18616

5 C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.50E-255//1179bp//99%/AF095192

C-HEMBA1003418//TRICHOHYALIN.//8.70E-19//281aa//31%/P37709

C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%/AB013139

10 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%/P00736

C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (TSLET-2).//8.80E-189//360aa//96%/P50480

C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.10E-68//251aa//52%/P53384

C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.20E-31//71aa//100%/P16874

15 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//7.90E-49//279aa//32%/P19474

C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.90E-206//445aa//74%/Q13330

C-HEMBA1003581//TALIN.//4.40E-45//52aa//98%/P26039

20 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.40E-10//118aa//35%/P19682

C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.//0//1713bp//99%/AB026125

C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.//6.90E-178//501bp//97%/AB015344

C-HEMBA1003645//TIPD PROTEIN.//2.40E-10//289aa//23%/O15736

25 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.20E-75//151aa//99%/Q13207

C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%/P23253

C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//423aa//47%/P34629

30 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2.00E-73//526aa//32%/Q13105

C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.10E-59//249aa//47%/P53973

C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//1.70E-44//501bp//67%/AF037339

35 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%/Q16665

C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//5.80E-81//511bp//86%/U17343

C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.10E-190//1204bp//84%/AF084259

40 C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.//0//988bp//95%/AF090402

C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%/P40484

C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//1.20E-105//1192bp//70%/AF030430

45 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.80E-16//89aa//46%/P16372

C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.50E-221//1188bp//78%/AF091234

C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.60E-166//416aa//72%/Q14141

C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//3.90E-208//951 bp//99%/AF067855

50 C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//8.40E-60//243aa//39%/P34529

C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.20E-30//208aa//37%/P51153

C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.50E-12//258aa//29%/P40991

C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%/AF074515

C-HEMBA1004208//Homo sapiens insulin-like growth factor receptor type 1 mRNA, complete cds.//1.50E-105//1192bp//99%/AF074516

C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6).//2.00E-43//98aa//84%/Q08755

- C-HEMBA1004275//Homo sapiens PHD-finger protein (GRC5) mRNA, complete cds.//1.10E-152//1403bp//69%//AF043725
- C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.80E-257//738bp//99%//AF092094
- 5 C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//0//1982bp//99%//AF022795
- C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103
- C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-93//357aa//42%//Q99676
- C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471
- 10 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516
- C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494
- C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1437bp//99%//AF125158
- 15 C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//3.20E-32//148aa//52%//P52017
- C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221
- C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333
- 20 C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//200aa//28%//Q13107
- C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2E-316//1445bp//99%//AF089841
- C-HEMBA1004573//Homo sapiens mRNA for HELG protein.//2.00E-59//483bp//68%//AJ277291
- 25 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844
- C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583
- C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//2.90E-05//303aa//21%//P35749
- 30 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
- C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds.//4.60E-109//650bp//89%//AB002405
- C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.10E-34//515bp//66%//U49082
- C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.60E-246//1249bp//94%//L39060
- 35 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.40E-111//314aa//58%//P08547
- C-HEMBA1004795//CDC4-UKE PROTEIN (FRAGMENT).//3.80E-69//198aa//66%//P50851
- C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.20E-154//317aa//94%//Q00004
- C-HEMBA1004889//Human C3f mRNA, complete cds.//6.70E-24//341aabbp//26%//U72515
- 40 C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.50E-05//148aa//24%//P25386
- C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa//100%//Q16401
- C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEURO FILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%//P12036
- 45 C-HEMBA1004973//ZINC-BINDING PROTEIN A337.//4.10E-08//121aa//33%//Q02084
- C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//0//1813bp//99%//AF041474
- C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947
- C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290
- 50 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//AF080561
- C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941
- C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//Q00004
- C-HEMBA1005206//Drosophila similans anap73B' gene and S. J. B. gene.//4.90E-111//172aa//54%//P12036
- C-HEMBA1005338//Homo sapiens mRNA for mamlin-4, partial cds.//3.90E-41//1095bp//99%//AF132947
- C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743
- C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//

AF071787

C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds//3.90E-126//1097bp//75%//AF200357

C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//2.00E-213//537bp//99%//AF041248

C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//1.90E-129//332aa//61%//O02193

C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1)//3.10E-154//285aa//99%//Q60809

C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds//0//1578bp//98%//AF191340

C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds//1.00E-220//1014bp//99%//AF134157

C-HEMBA1005558//NUCLEAR PROTEIN SNF7//6.40E-16//170aa//31%//P39929

C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds//1.20E-122//870bp//82%//D86949

C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds//0//1721bp//100%//AF133270

C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN)//0.00000009//213aa//27%//P09492

C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC)//2.30E-54//562aa//29%//P34036

C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA, complete cds//8.00E-211//962bp//99%//AF072933

C-HEMBA1005666//Homo sapiens mRNA for DIPB protein//8.60E-147//685bp//99%//AJ249128

C-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3)//2.10E-37//98aa//81%//Q15768

C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT)//4.40E-17//167aa//34%//P25296

C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE)//2.00E-36//342aa//33%//P00789

C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//5.60E-15//76aa//51%//P51522

C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0//2371bp//100%//AF082516

C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds//0//1413bp//99%//AB019435

C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT)//3.10E-33//81aa//64%//Q61001

C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds//8.20E-12//297bp//64%//AF098066

C-HEMBA1006130//SEL-10 PROTEIN//0.000000043//219aa//25%//Q93794

C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0//155 bp//99%//AF048693

C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR//1.90E-19//215aa//39%//P05142

C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)//8.60E-23//151aa//37%//P16372

C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR//0.00000002//62aa//53%//P42698

C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds//3.50E-157//845bp//92%//AF073836

C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-)//1.30E-123//200aa//73%//P10265

C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//1.00E-210//490aa//77%//P25500

C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2//0.000000012//176aa//30%//P32505

C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-)//4.20E-12//215aa//23%//P70473

C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds//5.30E-169//774bp//100%//AF005050

C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds//3.70E-225//1189bp//88%//AF076183

C-HEMBA1006344//RADIXIN//1.50E-31//333aa//28%//P26043

C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//1.80E-130//332aa//62%//O02193

C-HEMBA1006398//Human cytochrome c, putative, complete cds//2.00E-277//1729bp//85%//U33563

C-HEMBA1006445//Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds//1.40E-270//1224bp//

100%/U96750

C-HEMBA1006474//40 KD PROTEIN//1.40E-39//292aa//34%/Q01552

C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA)//1.90E-81//153aa//97%/P55786

5 C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2//1.40E-46//316aa//32%/O60879

C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)//4.00E-33//177aa//42%/P25716

C-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds//2.80E-206//1107bp//83%/U06944

10 C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds//1.70E-63//1002bp//65%/AF190774

C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG//0.00000069//109aa//38%/Q58323

C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC)//9.00E-40//113aa//82%/O15509

C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7//2.40E-44//206aa//47%/P14148

15 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION//3.30E-22//241aa//31%/P53196

C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT)//0.00000043//111aa//40%/Q01485

20 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds//0//1832bp//91%/AF152492

C-HEMBA1006807//Homo sapiens mRNA for SPOP//5.70E-125//1109bp//75%/AJ000644

C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN//2.00E-59//378aa//39%/P16256

C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds//0//1467bp//96%/AB018566

25 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds//0//1837bp//99%/U35832

C-HEMBA1006941//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds//2.10E-271//1234bp//99%/AF118649

30 C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//5.60E-143//740bp//94%/AF004828

C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/4)GlcNAc alpha-2,3-sialyltransferase//1.90E-80//447bp//89%/X74570

C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (UC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A)//2.40E-188//391aa//89%/Q90828

35 C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//8.30E-27//253aa//30%/Q10568

C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds//1.70E-252//1118bp//92%/AF125042

C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds//0//1900bp//99%/AF076929

40 C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//3.80E-271//642bp//99%/AF062085

C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds//0//1588bp//99%/AF139658

C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds//0//1590bp//99%/AF196304

45 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds//2.00E-58//650bp//70%/J00060

C-HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds//5.00E-58//330bp//95%/AF176707

C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds//0//1519bp//99%/AF127479

50 C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT)//6.20E-18//115aa//33%/P13941

C-HEMBA1000036//Homo sapiens CGI-51 protein mRNA, complete cds//0//1665bp//99%/AF151809

C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.80E-187//1582bp//80%/AF084928

C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE//2.40E-47//476aa//42%/U06944

C-HEMBA1000114//Homo sapiens ASM1 gene//0//1891bp//99%/U06944

C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24)//1.40E-24//71aa//77%/P51177



C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757  
 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738  
 C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete  
 cds.//3.00E-130//553bp//86%//AF062740  
 5 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//  
 27%//Q05481  
 C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092  
 C-HEMBB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-AT-  
 PASE M9.2 SUBUNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-32//80aa//78%//O15342  
 10 C-HEMBB1001673//Homo sapiens gene for new zinc finger protein, complete cds.//0//1919bp//99%//AB012770  
 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3  
 P110).//4.60E-15//391aa//25%//P55884  
 C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330  
 C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167  
 15 C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//0//  
 1514bp//99%//AF056209  
 C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//  
 P18720  
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//  
 20 241aa//48%//P47853  
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)  
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549  
 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709  
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//  
 25 874bp//86%//U47742  
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-  
 OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME  
 64E).//6.90E-132//561aa//50%//Q24574  
 C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.1.1.1) (COPROPORPHYRINOGENASE)  
 30 (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304  
 C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.70E-49//139aa//55%//P29981  
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715  
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163  
 C-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN  
 35 KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa//74%//P55144  
 C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//  
 44%//Q05481  
 C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737  
 C-HEMBB1002342//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//1.50E-229//  
 40 1045bp//99%//AF118649  
 C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692  
 C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885  
 C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365  
 C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E-28//266aa//33%//P27544  
 45 C-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//0//1417bp//99%//AF089749  
 C-HEMBB1002607//Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.//2.00E-  
 136//660bp//98%//AF105421  
 C-HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.//7.80E-285//841bp//96%//AF132961  
 C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//8.20E-198//868bp//99%//  
 50 Z47553  
 C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN  
 GP37].//1.90E-07//249aa//27%//P03396  
 C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%//P47226  
 C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C2856.96C.4EC.6.1.1.16. CYSTEINYL-  
 TRNA SYNTHETASE (CYS-TRNA-SYNTHETASE) (CYS-TRNA-SYNTHETASE) (CYS-TRNA-SYNTHETASE)  
 C-MAMMA1000113//Homo sapiens 5S ribosomal RNA (5S rRNA) (5S rRNA) (5S rRNA) (5S rRNA)  
 C-MAMMA1000164//Homo sapiens 5S ribosomal RNA (5S rRNA) (5S rRNA) (5S rRNA) (5S rRNA)  
 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//

C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//0//1466bp//99%/AB015132

C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds.//8.30E-178//1992bp//84%//AF195883

10 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.)/4.40E-33//250aa//  
33%//P42660

C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds.//0//2391bp//99%//  
AF172451

C-MAMMA1000713//L-RBULOKINASE (EC 2.7.1.16)//7.70E-17//246aa//29%//P94524

15 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//  
45%//O14646

C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779

C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1//9.00E-299//1033aa//55%//P87115

20 C-MAMMA1000824//ACTIN.//6.20E-20//284aa//28%/P53500

C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%//O27540

C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (TTI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033

C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8 //0//1767bp//99%//AJ250711

25 C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds.//2.50E-276//1263bp//99%//  
AF117892

C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT)//1.20E-26//276aa//28%//Q90674

30 C-MAMMA1001038/MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN/2.60E-107/190aa/95%/Q15746

C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%//Q01082

C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5//0//1440bp//99%/AJ237946

C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds//1.30E-181//397bp//98%//AF151830

C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//  
AF067420

C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%/P51521

C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%/Q09273

C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338

40 C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds.//0//2253bp//99%//AB015346

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%/P12978

C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.//2.30E-271//1414bp//89%//AF184275

45 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.10E-52//630aa//  
30%/P34537

C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)  
(RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)  
(P50-RHOGAP).//2.20E-98//283aa//63%//Q07960

50 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)//0.000000017//46aa//60%//P20931

C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)//1.40E-165//312aa//99%/P02750

C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT)//6.50E-129//260aa//92%/P52623

C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED A

**GAMMA**™ 10-26 mmHg 14mmHg tubing (MNH) complete cds + 50E-275 + 55 lpp (90% Mn)

MAMMA1001b27/Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%[A.J007989](#)

2-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%/P49910

C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ)//0.00000058//29aa//100%//P47756  
 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687  
 C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V)//5.90E-240//445aa//97%//P09653  
 5 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR)//8.50E-32//171aa//36%//P21573  
 C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708  
 C-MAMMA1001754//Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA complete cds.//0//1987bp//99%//AF112204  
 10 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156//3.80E-45//351aa//38%//Q58556  
 C-MAMMA1001771//M.musculus mRNA for semaphorin B//2.60E-200//1272bp//79%//X85991  
 C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148  
 15 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29)//2.60E-77//507aa//38%//Q07230  
 C-MAMMA1001868//TRICHOHYALIN//2.70E-19//359aa//25%//P22793  
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%//AF099664  
 C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)//6.00E-66//157aa//70%//P15880  
 20 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B)//5.20E-61//60aa//90%//P32119  
 C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.30E-181//861bp//98%//AF032667  
 C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)//8.80E-217//310aa//86%//PP70541  
 25 C-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.00E-190//1624bp//76%//AF068748  
 C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.10E-214//881bp//97%//AJ011679  
 30 C-MAMMA1002329//M.musculus mRNA for semaphorin B//3.80E-45//332bp//84%//X85991  
 C-MAMMA1002351//Mus musculus dynactin subunit p25 (p25) mRNA, complete cds.//4.30E-119//773bp//86%//AF190795  
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D//1.50E-07//206aa//29%//Q02926  
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2)//1.10E-24//96aa//68%//Q14108  
 35 C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)//1.00E-11//128aa//36%//P47623  
 C-MAMMA1002485//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//1822bp//99%//AF098462  
 40 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.20E-34//337aa//31%//P43571  
 C-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//0//1910bp//99%//AF065214  
 C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//2.60E-19//666aa//23%//P08640  
 45 C-MAMMA1002617//ZINC FINGER PROTEIN 135//7.60E-89//252aa//57%//P52742  
 C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)//9.50E-16//159aa//37%//Q09931  
 50 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640  
 C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC)//1.30E-198//550aa//70%//Q07866  
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030  
 C-MAMMA1002655//Homo sapiens mRNA for ganglioside sialidase, complete cds.//0//1515bp//99%//AB008185  
 C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE COA LIGASE) (ACYL-CoA SYNTHETASE)  
 C-MAMMA1002699//Rattus norvegicus mRNA for semaphorin B//2.60E-200//1272bp//79%//X85991  
 42bp//85%//AF018261  
 C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.//

2.20E-25//330bp//77%//AF011794

C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//2.60E-58//373bp//81%//U58883

C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)//4.90E-10//334aa//22%//P52178

C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590

C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//1.40E-160//305aa//85%//P48059

C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.70E-30//214aa//35%//P48060

C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742

C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343

C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.70E-123//370aa//66%//Q02874

C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.40E-46//332aa//36%//P06746

C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.90E-13//108aa//33%//P23851

C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//1533bp//99%//AF077952

C-MAMMA1003057//MD6 PROTEIN.//3.10E-225//419aa//97%//Q60584

C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.10E-234//1178bp//86%//AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.20E-105//217aa//89%//P46735

C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.30E-218//996bp//99%//Y15062

C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//5.00E-13//592aa//24%//P47179

C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//3.10E-158//592bp//97%//AF123052

C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110

C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596

C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//0//3106bp//89%//D87671

C-NT2RM1000080//UNC-1 PROTEIN.//5.90E-25//211aa//31%//Q21190

C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//8.40E-52//364aa//32%//P34537

C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843

C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072

C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.80E-110//516bp//99%//AF044959

C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.30E-38//469aa//27%//P49902

C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072

C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.10E-10//94aa//47%//O42643

C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//AJ245820

C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.//2.00E-126//592bp//99%//U81002

C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.70E-35//569bp//64%//X73882

C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//3012bp//99%//AB016789

C-NT2RM1000257//MAGO NASHI PROTEIN.//7.90E-69//143aa//91%//P49028

C-NT2RM1000260//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//AF055995

C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.50E-106//118aa//97%//P39942

- C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//7.40E-245//2101bp//68%//AF111423
- C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.//7.0//1599bp//99%//AF152462
- 5 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.//3.20E-196//1016bp//94%//AF179212
- C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000019//67aa//31%//P53915
- C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 10 C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.40E-185//1486bp//81%//AF084928
- C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.//3.00E-17//927bp//58%//AJ132700
- C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
- C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731
- 15 C-NT2RM1000555//UNR PROTEIN.//0//678aa//98%//P18395
- C-NT2RM1000563//TRANSMISSION-B LOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372
- C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 20 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
- C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds.//5.70E-210//960bp//99%//AF038957
- C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.20E-09//165aa//34%//P16989
- C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
- 25 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695
- C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
- C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.//6.70E-227//1043bp//99%//AF141310
- 30 C-NT2RM1000770//DXS6673E PROTEIN.//1.40E-39//194aa//48%//Q14202
- C-NT2RM1000772//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//7.30E-15//280aa//27%//Q00808
- C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.10E-98//571bp//89%//Z97207
- C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
- 35 C-NT2RM1000826//UNR PROTEIN.//0//678aa//98%//P18395
- C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541 bp//99%//AF08445 8
- C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.70E-42//333aa//36%//P16157
- C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//0//2206bp//99%//AF077033
- 40 C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.40E-244//1113bp//99%//AF043733
- C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//4.30E-122//1394bp//69%//AF126799
- 45 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516
- C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.80E-56//630aa//30%//P34537
- C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700
- 50 C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//8.90E-26//229aa//29%//P02583
- C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.00E-15//266aa//26%//P46577
- C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds.//0//2230bp//99%//AF082516
- C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//

Q99383

C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODEESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//8.30E-47//259aa//35%//P08487

5 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%//Q05481

C-NT2RM1001102//Human HEM45 mRNA, complete cds.//2.30E-27//482bp//63%//U88964

C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//5.60E-06//239aa//27%//P54197

10 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.20E-144//362aa//71%//P25167

C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703

15 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOL ESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.30E-36//160aa//40%//P50102

C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.60E-19//181aa//34%//P14918

20 C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTRANSFERASE).//8.10E-06//167aa//29%//O48660

C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.80E-14//245aa//29%//P11274

C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251

25 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE).//1.70E-68//419aa//36%//P50849

C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.60E-54//344aa//33 %//P32802

30 C-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//9.70E-201//826bp//84%//AF030430

C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1.00E-222//237aa//89%//Q08469

C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.00E-07//157aa//28%//P36113

35 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//8.90E-06//377aa//24%//P22211

C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.80E-13//166aa//34%//P41823

C-NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.//1.70E-58//381bp//86%//U78304

C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243

40 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.30E-12//282aa//32%//P17437

C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//0//2519bp//96%//AF032108

C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.70E-187//741aa//46%//P73505

45 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.80E-60//384aa//40%//P53973

C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487

C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.90E-70//838bp//69%//AF179221

50 C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp//99%//AJ245620

C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//2.60E-106//1069bp//74%//U35776

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%//Q08170

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%//Q08170

C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%//Q08170

C-NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.//0//1731bp//99%//AF121141

C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//2.90E-103//249aa//73%//P28160  
 C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L//5.70E-53//266aa//43%//  
 P41877  
 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)//9.50E-279//545aa//  
 5 98%//P23514  
 C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//1.70E-200//927bp//99%//  
 AB015046  
 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1)//8.20E-154//285aa//99%//Q60809  
 C-NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds//0//1554bp//99%//AF100757  
 10 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III//2.40E-15//266aa//  
 26%//P46577  
 C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds//1.20E-28//805bp//61%//  
 AF053091  
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.30E-20//267aa//35%//P05143  
 15 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)//1.50E-07//95aa//35%//  
 P48724  
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)//3.60E-10//  
 177aa//32%//P97924  
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
 20 DOHYDROLASE)//1.30E-180//328aa//99%//P13264  
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR)//1.60E-166//312aa//98%//  
 P53995  
 C-NT2RM2001324//ZYXIN//6.80E-55//200aa//41%//Q04584  
 C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//2.90E-08//334aa//22%//Q00808  
 25 C-NT2RM2001424//Homo sapiens mRNA for EIB-55kDa-associated protein//0//1621bp//99%//AJ007509  
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2)//7.40E-121//  
 437aa//57%//P52569  
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//6.90E-27//  
 90aa//42%//P38660  
 30 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//  
 4.30E-61//312aa//44%//P19474  
 C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds//3.10E-156//909bp//88%//AF032667  
 C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein//0//3114bp//99%//AJ132440  
 C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds//0//2601 bp//99%//AF084458  
 35 C-NT2RM2001632//KES1 PROTEIN//1.40E-31//342aa//34%//P35844  
 C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PRO-  
 TEIN OF 121 KD) (P145)//1.20E-142//566aa//56%//P52591  
 C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds//0//2421 bp//99%//AF084458  
 C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds//0//2608bp//99%//  
 40 AF111162  
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN//3.40E-39//161aa//34%//P20107  
 C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA complete cds//0//  
 2471bp//99%//AF044195  
 C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in  
 45 intron 11, complete cds//6.20E-16//464bp//62%//AFQ83391  
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29)//6.50E-104//407aa//43%//Q07230  
 C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds//0//  
 1843bp//94%//U21155  
 50 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I//4.60E-20//253aa//  
 30%//Q09674  
 C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds//6.20E-253//  
 1170bp//99%//AB028600  
 C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD)  
 (FRAGMENT)//5.70E-130//536aa//49%//P50544  
 C-NT2RM2001701//Homo sapiens mRNA for ubiquitin carboxyl-terminal hydrolase K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-

ZYME)//7.20E-16//381aa//27%//Q09931

C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//0//1498bp//99%//AF011792

C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.80E-11//119aa//36%//Q92609

5 C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds.//0//2379bp//99%//AF084458

C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.40E-154//394aa//64%//P52742

C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.//0//1470bp//99%//AF135422

10 C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2150bp//99%//AF126799

C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195

C-NT2RM2001823//CHD1 PROTEIN.//1.80E-106//631aa//39%//P32657

C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//97%//AF013759

15 C-NT2RM2001886//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//3.00E-54//337aa//39%//P53010

C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.10E-26//204aa//34%//P28692

C-NT2RM2001930//M.musculus mRNA for semaphorin G.//5.20E-135//894bp//83%//X97818

20 C-NT2RM2001935//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//0//1454bp//99%//AF125182

C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.70E-27//216aa//34%//P28320

C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250

25 C-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//0//1658bp//98%//AF089816

C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.90E-39//253aa//35%//P37838

30 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa//28%//Q12730

C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME L//3.10E-12//206aa//30%//Q09782

C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.90E-08//83aa//44%//P40796

35 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.10E-89//425aa//41%//P46837

C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789

40 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878

C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5.00E-62//104aa//57%//Q61990

C-NT2RM2002091//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//7.10E-29//805bp//61 %//AF053091

45 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840

C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435

C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.90E-13//487aa//26%//P49695

50 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8.00E-31//105aa//47%//P47805

C-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//8.50E-191//1524bp//81%//AF084928

C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2) //7.10E-155//381aa//72%//P25167

C-NT2RM4000046//GOLGI APPARATUS PROTEIN 1 (GOLGI APPARATUS PROTEIN 1) //0.0000008 //104aa//100%//P52742

C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81//251aa//53%//P52742

C-NT2RM4000139//R.norvegicus trg mRNA.//2.30E-114//1161bp//72%//X68101

C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA  
 LIGASE) (THRRS)//1.20E-157//321aa//61%//P26639  
 C-NT2RM4000156//H.sapiens HPBRII-7 gene//3.60E-21//785bp//60%//X67336  
 C-NT2RM4000167//Homo sapiens mRNA for Chromokinesin (KIF 4 gene)//0//1946bp//99%//AJ271784  
 5 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//4.80E-13//686aa//23%//  
 P25386  
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10//9.20E-75//439aa//41%//P16381  
 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2)//4.90E-32//170aa//41%//Q16600  
 C-NT2RM4000215//MAK16 PROTEIN//1.30E-68//295aa//49%//P10962  
 10 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds//1.10E-27//  
 633bp//64%//L20303  
 C-NT2RM4000233//Mus musculus semaphorin Via mRNA, complete cds//3.40E-231//1395bp//86%//AF030430  
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.20E-276//1124bp//  
 97%//M99438  
 15 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L//0//2030bp//99%//  
 AJ132637  
 C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN)//1.50E-21//208aa//35%//Q24371  
 C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17//5.90E-80//213aa//75%//P35292  
 C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds//0//2156bp//87%//AF195418  
 20 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor//0//1730bp//99%//AJ133769  
 C-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds//4.10E-271//  
 2085bp//77%//AF062476  
 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I//8.00E-20//393aa//  
 24%//Q10297  
 25 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds//0//2092bp//99%//AF097025  
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CON-  
 TAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//4.80E-11//242aa//31%//P04280  
 C-NT2RM4000496//SAP1 PROTEIN//8.30E-53//434aa//29%//P39955  
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)  
 30 (FRAGMENT)//1.10E-11//394aa//24%//P16884  
 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29)//2.40E-89//389aa//43%//Q07230  
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN)//1.00E-59//595aa//28%//Q04652  
 C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN//8.70E-15//403aa//30%//  
 P26337  
 35 C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//2.90E-09//108aa//31%//Q00808  
 C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-  
 TIVATING ENZYME)//2.70E-146//420aa//60%//P27550  
 C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC  
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III)//3.00E-68//297aa//40%//P51178  
 40 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL13747//1.20E-28//180aa//30%//P74168  
 C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.00E-136//  
 1104bp//77%//AF022789  
 C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO//0.00000041//207aa//29%//P52154  
 C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds//0//2071bp//  
 99%//AF221712  
 45 C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1p, complete cds//0//2184bp//99%//D88208  
 C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT)//3.90E-125//301aa//53%//Q99676  
 C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete  
 cds//0//2603bp//99%//AF084521  
 50 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE  
 AC45 SUBUNIT)//1.10E-24//138aa//44%//P40682  
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)//6.70E-22//250aa//29%//P02750  
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//8.00E-211//738aa//  
 50%//Q05481  
 C-NT2RM4001054//Homo sapiens secretin homolog mRNA, complete cds//0//1481bp//99%//AF077777  
 C-NT2RM4001084//HYPOTHETICAL 135.6 KD PROTEIN C16C9.06C IN CHROMOSOME I//0.000000032//  
 165aa//33%//Q09820

C-NT2RM4001092//ZINC FINGER PROTEIN GLO37/3.10E-24//265aa//33%/P38682  
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II//5.90E-86//292aa//48%/Q09417  
 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D//1.00E-11//103aa//38%/Q01704  
 5 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN//4.10E-197//445aa//78%/Q27969  
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1//1.10E-48//218aa//43%/Q03532  
 C-NT2RM4001200//ZINC FINGER PROTEIN 135//9.50E-135//375aa//60%/P52742  
 C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//0//2310bp//99%/AF004828  
 10 C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds//3.10E-148//1445bp//72%/U65079  
 C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds//4.30E-55//289bp//77%/AF129131  
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-UKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)//3.50E-35//124aa//65%/P54676  
 15 C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD)//2.30E-31//334aa//30%/P08503  
 C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds//1.80E-39//728bp//64%/D89016  
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN)//1.00E-28//171aa//37%/P32626  
 20 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION//8.10E-30//265aa//33%/P53742  
 C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds//0//2300bp//99%/AF155103  
 C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds//0//2524bp//99%/AB019494  
 C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//2.20E-237//1079bp//99%/AF098799  
 25 C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds//0//1962bp//87%/AF020526  
 C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds//0//1918bp//99%/AF047711  
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//1.40E-118//444aa//46%/P73505  
 30 C-NT2RM4001483//ZINC FINGER PROTEIN 136//5.10E-106//357aa//55%/P52737  
 C-NT2RM4001566//NECDIN//9.80E-44//227aa//41%/P25233  
 C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds//1.50E-284//1082bp//90%/AF071317  
 35 C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION//7.60E-56//213aa//49%/P31380  
 C-NT2RM4001597//M.musculus red-1 gene//12.10E-171//1414bp//78%/X92750  
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)//2.60E-32//203aa//39%/Q12600  
 C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3)//1.50E-93//278aa//38%/Q13368  
 40 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION//2.70E-84//410aa//42%/P37339  
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT)//8.90E-141//354aa//72%/Q14141  
 C-NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds//0//1922bp//100%/AF179221  
 45 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.)//4.10E-186//639aa//58%/Q05512  
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1)//7.90E-66//311aa//35%/Q03164  
 C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1)//5.10E-07//263aa//30%/P16112  
 50 C-NT2RM4001813//LECTIN BRA-2//0.00000048//114aa//30%/P17346  
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds//8.10E-300//1395bp//98%/M37712  
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT)//6.50E-22//126aa//46%/P79779

C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.30E-244//1248bp//94%//Y17711

C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa//36%//Q15404

5 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%//P47486

C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.//0//1930bp//99%//AF102851

C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//0//2087bp//99%//AF098162

C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.60E-261//1563bp//84%//X99330

10 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%//P51523

C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%//P16170

15 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//6.90E-94//589aa//35%//P42935

C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.90E-53//1585bp//60%//AF104260

C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//1.90E-31//80aa//52%//P36419

20 C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//1865bp//99%//U82267

C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71 %//AF117755

C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//AF072758

25 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41 %//Q04652

C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//2550bp//99%//AF176085

C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%//AJ271784

C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014

30 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940

C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%//AF084535

C-NT2RM4002174//MRPPROTEIN.//9.10E-68//264aa//51%//P21590

C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%//P08640

35 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430

C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa//72%//Q07803

C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.//0//2452bp//100%//AF157028

40 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%//P40809

C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYLOLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.20E-36//320aa//38%//P27808

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%//P48778

45 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.30E-29//275aa//30%//P27095

C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.10E-49//611 bp//70%//AF129131

50 C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%//P51515

C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%//Q00808

C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%//P55137

C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%//AF055899

C-NT2RM4002571

C-NT2RM4002571//Homo sapiens mRNA for UDP-GlcNAc 6-epimerase.//1.50E-78//921bp//69%//X85011

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%//P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA UGASE) (ASPRS).//  
2.30E-101//488aa//45%//O32038

C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//0//1747bp//99%//AB013385

C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1652bp//99%//AJ012449

5 C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%//  
AF193608

C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834

C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4.00E-116//296aa//51%//P93471

C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.50E-50//181aa//60%//P51859

10 C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270//  
951bp//98%//AF011792

C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%//Q02357

C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267//  
1155bp//87%//AB015895

15 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-  
plete cds.//1.30E-275//1249bp//99%//AF053551

C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.70E-47//155aa//58%//P32447

C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.70E-15//162aa//30%//P25343

C-NT2RP1000363//R.norvegicus LL5 mRNA77.90E-262//1175bp//83%//X74226

20 C-NT2RP1000376//Homo sapiens Ca2+-independent phospholipase A2 long isoform (iPLA2) mRNA, complete  
cds.//0//2252bp//96%//AF102989

C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.90E-153//230aa//99%//  
P55161

C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-  
94//1019bp//63%//AF111423

25 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-  
CRYSTALLIN).//2.40E-10//227aa//25%//Q08257

C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//3.80E-19//149aa//36%//P17624

C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.60E-94//  
30 254aa//47%//P34580

C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.50E-240//445aa//97%//P09653

C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//7.5e-315//1445bp//99%//  
AF039688

C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM  
35 GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//3.60E-30//534aa//23%//P33194

C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%//U47101

C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-  
OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-  
ZYME 1).//8.20E-83//345aa//47%//Q61068

40 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.10E-  
27//193aa//35%//P49020

C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.50E-75//151aa//94%//  
P97367

C-NT2RP1000630//NECDIN.//2.40E-44//227aa//41%//P25233

45 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-  
PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721

C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//  
1687bp//99%//AF145020

C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%//E14379

50 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete  
cds.//0//2186bp//99%//AF101434

C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//  
99%//AF173378

C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-  
OPROTEIN 2) (CD62E) (ALPHA-2B-Glycoprotein IIb/IIIa) (B32) (B3) (B2) (B1) (B0)

C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE-  
ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.20E-83//334aa//50%//Q07960

C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//

AF067223

C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020

C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)//1.20E-30//232aa//30%//O35566

C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//33%//Q09531

C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%//Q13823

C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.60E-105//504bp//99%//U39317

C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN)//1.40E-23//370aa//28%//Q04652

C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%//Q13823

C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.50E-236//966bp//99%//M17885

C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-299//554aa//99%//P19338

C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.20E-78//1529bp//61%//L01790

C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522

C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%//AF201333

C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.10E-107//504bp//99%//AF182291

C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//U82267

C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001113//Homo sapiens CTL2 gene.//0//2790bp//98%//AJ245621

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139

C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513

C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%//AF029914

C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001310//Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product.//0//1732bp//99%//AF176006

C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799

C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//6.50E-116//541bp//100%//AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.70E-22//284aa//25%//P40074

C-NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1782bp//99%//AF210052

C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.90E-141//396aa//67%//P91917

C-NT2RP1001449//Mus musculus Gng31g mRNA, complete cds.//7.20E-165//800bp//87%//AF069954

C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.20E-137//629bp//100%//AJ005257

C-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//2.10E-158//755bp//86%//L11316

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.20E-40//261aa//27%//Q08891

C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803

C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN) (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)

C-NT2RP1001547//HOMO SAPIENS G-PROTEIN COUPLING RECEPTOR PETA-3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN) (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)

C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594

C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40)//9.80E-17//79aa//  
 55%//O34136  
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.40E-177//726aa//47%//  
 P51523  
 5 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//7.1.80E-22//184aa//  
 34%//Q01730  
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//  
 0//1390bp//98%//AF061749  
 10 C-NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.//0//  
 2245bp//99%//AF155109  
 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-  
 SILON)//9.40E-16//45aa//100%//P49446  
 C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3546bp//99%//AF195418  
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//3.40E-51//  
 15 383aa//32%//P33450  
 C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene)//7.90E-20//265bp//73%//  
 AJ242730  
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356  
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L//2.50E-117//541aa//42%//  
 20 P41877  
 C-NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//1490bp//99%//  
 AF175966  
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN  
 AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN  
 25 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)//4.40E-226//423aa//99%//P35585  
 C-NT2RP2000153//GAR2 PROTEIN//9.80E-23//311aa//28%//P41891  
 C-NT2RP2000157//MLO2 PROTEIN//2.60E-11//62aa//40%//Q09329  
 C-NT2RP2000161//DIS3 PROTEIN HOMOLOG//4.10E-35//184aa//44%//Q17632  
 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN  
 30 NSP60)//3.30E-16//114aa//44%//O02675  
 C-NT2RP2000195//Homo sapiens androgen induced protein (AIG-1) mRNA, complete cds.//7.80E-152//704bp//  
 99%//AF153605  
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1)//0.000043//103aa//28%//P35568  
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE  
 35 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT)//3.40E-21//210aa//33%//P56558  
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W//9.70E-41//278aa//36%//P40556  
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (AI 140 KD  
 SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA)//  
 7.10E-12//213aa//23%//P35251  
 40 C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds.//1.30E-242//  
 1043bp//99%//U78723  
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I//1.60E-27//576aa//  
 25%//Q10297  
 C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT)//3.30E-186//256aa//60%//Q99676  
 45 C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.30E-279//  
 1193bp//99%//U82381  
 C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//2.00E-111//  
 226aa//92%//P08760  
 C-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//0//2331bp//  
 50 99%//U83981  
 C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//0//1886bp//99%//L28010  
 C-NT2RP2000420//ZINC FINGER PROTEIN 165//8.50E-33//155aa//52%//P49910  
 C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//  
 99%//AF102265  
 C-NT2RP2000523//Homo sapiens N-acetylglucosamine-6-phosphate 4-epimerase mRNA, complete cds.//0//  
 1412bp//99%//AF141238  
 C-NT2RP2000660//SAP1 PROTEIN//5.20E-68//474aa//32%//P39955

C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//1.30E-27//349aa//32%//Q01577

C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.70E-100//488aa//44%//O32038

5 C-NT2RP2000764//NIFS PROTEIN//6.60E-36//252aa//42%//P12623

C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds//0//3347bp//99%//AF095195

C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A)//5-.60E-08//179aa//29%//Q99104

10 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120)//1.10E-07//96aa//29%//P13466

C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT//7.90E-08//172aa//28%//P26174

C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//0//1562bp//99%//U80811

15 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2//0//694aa//99%//O60841

C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds//2.90E-191//1094bp//85%//AB006135

C-NT2RP2000931//MATRIN 3//2.40E-289//467aa//95%//P43244

C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds//0//2767bp//99%//AF130464

C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds//0//1989bp//96%//AB024704

20 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE)//5.80E-46//222aa//45%//Q20939

C-NT2RP2001081//SYNAPTOTAGMIN IV//4.20E-118//430aa//54%//P50232

C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein//0//2514bp//99%//AJ132440

C-NT2RP2001168//VERPROLIN//1.50E-09//143aa//33%//P37370

25 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLGCF46.1 (FRAGMENT)//6.00E-10//88aa//38%//P18722

C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//2.00E-128//409aa//45%//Q05481

C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC)//2.20E-10//366aa//28%//P14105

30 C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT)//4.40E-91//179aa//99%//P28663

C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN//8.30E-39//161aa//34%//P20107

C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)//5.50E-116//311aa//71%//Q13829

35 C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//2.00E-11//403aa//25%//Q02817

C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)//8.40E-192//581aa//54%//P93647

C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein//0//2068bp//99%//Y18004

40 C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds//1.9e-316//1428bp//100%//AB020981

C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds//9.00E-112//742bp//82%//U76759

C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds//0//3712bp//99%//AB024334

C-NT2RP2001460//TRICHOHYAUN//1.00E-14//521aa//24%//P37709

C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds//3.20E-297//2206bp//75%//AF093097

45 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//0//2502bp//99%//Y14494

C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//0//2326bp//99%//AF035586

C-NT2RP2001560//VAV2 PROTEIN//0.00000015//219aa//27%//Q60992

50 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME 1//8.20E-29//294aa//31%//Q09837

C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE//0.000000036//127aa//36%//P30957

C-NT2RP2001601//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds//0//1748bp//99%//AF196304

C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds//0//2445bp//99%//U97067

C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-

NA, complete cds.//0//1287bp//99%//AF058718

C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE), (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.10E-47//126aa//53%//P42897

C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1)//7.90E-52//220aa//44%//Q61068

C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//797%//P14324

C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523

C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009

C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754

C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008

C-NT2RP2001883//Homo sapiens CGI-01- protein mRNA, complete cds.//0//2306bp//99%//AF132936

C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161

C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38//395aa//30%//P53946

C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.70E-177//1538bp//74%//AF062378

C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.//2.00E-38//435bp//67%//AF090989

C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.50E-129//279aa//85%//Q08469

C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.70E-47//247aa//52%//P35331

C-NT2RP2002046//Homo sapiens mRNA for transcription factor.//0//1664bp//99%//AJ130894

C-NT2RP2002058//Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.//0//2510bp//99%//AF083217

C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306

C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa//32%//P18490

C-NT2RP2002079//HISTONE H1, GONADAL.//4.40E-11//214aa//34%//P02256

C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//33 89bp//99%//AJ007509

C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634

C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//4.30E-44//155aa//37%//Q13107

C-NT2RP2002185//Homo sapiens ubiquitin mRNA, complete cds.//0//1789bp//99%//AF176069

C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds.//0//2809bp//99%//AB021868

C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.//0//3118bp//91%//L38621

C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418

C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%//P42568

C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521

C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.40E-254//1158bp//99%//AB015594

C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.30E-240//1105bp//99%//AF038958

C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein.//3.20E-210//1136bp//93%//AJ242972

C-NT2RP2002442//HESA PROTEIN.//2.80E-14//163aa//30%//P46037

C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//6.50E-07//171aa//27%//P30620

C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%//U87306

C-NT2RP2002500//Homo sapiens mRNA for transcription factor HFX-B (HFXB) mRNA, complete cds.//3.70E-34//668bp//91%//AF105427

C-NT2RP2002520//Homo sapiens transcription factor HFX-B (HFXB) mRNA, complete cds.//3.70E-34//668bp//91%//AF105427

- C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.20E-19//288aa//26%/Q11073
- C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%/P51523
- 5 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.50E-35//181aa//42%/P12815
- C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%/U19181
- C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%/P19076
- 10 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.).//1.70E-51//326aa//38%/P55345
- C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.90E-14//210aa//30%/O14345
- C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.90E-85//489aa//43%/P55194
- 15 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%/AF041107
- C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%/D89016
- C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.80E-10//203aa//27%/P29764
- C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%/P14922
- 20 C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.90E-136//623bp//100%/AF038392
- C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.10E-87//395aa//40%/Q18964
- C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.40E-70//282aa//42%/P52737
- 25 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.60E-80//147aa//100%/P51669
- C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.00E-08//98aa//36%/P10129
- C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%/AB026190
- 30 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%/P70700
- C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//L90E-11//132aa//38%/Q13829
- C-NT2RP2003121//Mus musculus enhancer of polycbmb (Epc1) mRNA, complete cds.//2.30E-82//642bp//68%/AF079765
- 35 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.40E-38//539aa//25%/Q04652
- C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%/P13117
- C-NT2RP2003157//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.30E-13//185aa//38%/Q08170
- 40 C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//0//2091bp//99%/D67025
- C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%/AJ132545
- C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds.//0//1641bp//99%/AF006264
- C-NT2RP2003228//H.sapiens PI-Cdc21 mRNA.//0//2870bp//98%/X74794
- 45 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%/AF023657
- C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%/AJ242978
- C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%/AF151811
- 50 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%/AF176069
- C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.90E-16//145aa//43%/P30771
- C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'- PHOSPHATE CYCLASE) (RNA CYCLASE).//4.20E-88//374aa//47%/Q23400
- C-NT2RP2003295//Homo sapiens mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%/AJ242978
- C-NT2RP2003307//KINESIN 10.//2.20E-199//550aa//70%/Q07866
- C-NT2RP2003308//CROOKED NECK PROTEIN.//5.40E-244//622aa//67%/P17886



P39702

C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)//  
2.30E-53//141aa//78%//P20290

C-NT2RP2004041//SYNAPSINS IA AND B//0.00000074//159aa//32%//P17599

5 C-NT2RP2004066//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds//2.70E-288//  
1994bp//81%//AF156529C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-  
SE)//5.40E-30//319aa//31%//Q01513

C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein//1.10E-138//1236bp//74%//Y12781

10 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49)//  
5.60E-31//424aa//28%//Q07231C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds//3.80E-52//397bp//82%//  
AF00399815 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds//0//2272bp//99%//  
AB015982

C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds//0//3044bp//99%//AB015718

C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//  
9.90E-12//427aa//26%//P1924620 C-NT2RP2004245//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds//6.40E-117//  
1122bp//72%//AF200357

C-NT2RP2004270//PROTEIN PTM1 PRECURSOR//1.40E-16//334aa//24%//P32857

C-NT2RP2004366//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS 13//1.30E-51//505aa//  
29%//Q0787825 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR//9.30E-15//  
126aa//39%//P38120

C-NT2RP2004392//MNN4 PROTEIN//1.40E-11//143aa//27%//P36044

C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds//5.40E-243//1108bp//  
99%//AB028069

C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds//0//2321bp//86%//AF155739

30 C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds//0//2075bp//99%//AF180920

C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds//0//1387bp//86%//  
AF090190C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03//3.00E-117//625aa//40%//  
Q0990335 C-NT2RP2004587//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)//  
7.30E-07//352aa//23%//P07197

C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.50E-233//1061bp//99%//AJ006291

C-NT2RP2004681//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//  
2.60E-07//426aa//23%//P1924640 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I//5.60E-64//616aa//  
33%//Q92355C-NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds//1.50E-280//1464bp//85%//  
U4075045 C-NT2RP2004732//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)//  
7.30E-07//352aa//23%//P07197C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1)//1.30E-  
26//190aa//41%//P38692C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA  
LIGASE) (LEURS)//9.50E-73//153aa//59%//Q1049050 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC  
6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA)//3.70E-135//414aa//62%//P53588

C-NT2RP2004816//H58 PROTEIN//9.00E-173//327aa//98%//P40336

C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-  
CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN) //4.20E-09//804aa//  
Q81681

C-NT2RP2004933//Homo sapiens mRNA for E-kinase, complete cds//0.52103bp//99%//AB001113

C-NT2RP2004959//P54 PROTEIN PRECURSOR//0.00000095//297aa//20%//P13692

C-NT2RP2004961//Hattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds//1.00E-

228//1666bp//75%//U56732

C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.30E-47//353aa//30%//Q12386

C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//1.80E-99//376aa//43%//P19474

5 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779

C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.30E-47//155aa//59%//P32447

C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4.00E-91//218aa//44%//Q92089

10 C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA).//2.00E-173//273aa//57%//P34466

C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743

15 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921

C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//0.00E-01//1437bp//98%//AF045583

C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//0//1615bp//99%//AF005050

C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509

20 C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1N subunit (SUA1) mRNA, complete cds.//0//1262bp//99%//AF090385

C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025

C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053

25 C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//0//2992bp//99%//AF060219

C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170//780bp//100%//AF036144

C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//99%//AF124735

30 C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709

C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//38%//P32660

C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247

35 C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SEN1) mRNA, complete cds.//1.30E-52//753bp//67%//AF149770

C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.20E-39//224aa//35%//Q13823

C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059

40 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.20E-13//185aa//38%//Q08170

C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.//4.10E-202//962bp//98%//AF113540

C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-130//608bp//99%//AF070652

45 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3.00E-44//252aa//41%//P38127

C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032

C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.//1.80E-175//1102bp//83%//AF053628

C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418

50 C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742

C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PP2A).//5.20E-81//166aa//88%//P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803

C-NT2RP2005520//Homo sapiens chromosome-associated protein-F (hCAP-F) mRNA, complete cds.//0//1419bp//99%//AF069258

C-NT2RP2005525//Mus musculus Hsp adaptin mRNA, complete cds.//1.40E-104//1687bp//88%//AF039437

C-NT2RP2005531//PROTEIN 4.3BAND 4.3 (P4.3).//5.50E-70//393aa//39%//P11171

C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1560bp//98%//AJ012449

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)//2.00E-20//181aa//36%//Q39366

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds//1.00E-46//576bp//70%//AF062529

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)//8.20E-23//164aa//28%//O32053

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds//8.9e-313//1455bp//98%//AF062085

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)//1.00E-11//128aa//36%//P47623

C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1)//1.20E-13//74aa//45%//P56101

C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds//1.60E-248//1129bp//99%//AF043733

C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//4.40E-200//908bp//99%//AF089814

C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR//2.60E-10//175aa//27%//Q92834

C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN)//3.00E-63//323aa//39%//Q62158

C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds//0//2681 bp//99%//AF132022

C-NT2RP2005719//GPI-ANCHORED PROTEIN P137//4.00E-14//99aa//43%//Q14444

C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds//0//2545bp//99%//AB011414

C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN)//3.00E-09//169aa//28%//P38074

C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//0//1968bp//99%//AF068868

C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0//1966bp//99%//AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)//1.70E-61//374aa//38%//P47943

C-NT2RP2005767//G.gallus PB1 gene//5.00E-163//1158bp//81%//X90849

C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds//2.70E-180//656bp//99%//AF151351

C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP)//2.10E-213//249aa//85%//Q02038

C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//4.40E-55//358aa//42%//P51005

C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds//0//2191bp//92%//AF155120

C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION//2.30E-39//318aa//31%//P40004

C-NT2RP2005835//SHP1 PROTEIN//1.80E-28//208aa//32%//P34223

C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds//3.50E-52//1091bp//59%//AB039669

C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57)//5.00E-11//155aa//34%//P48837

C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//1.50E-67//388aa//44%//P25500

C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//1.50E-13//185aa//38%//Q08170

C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds//5.80E-120//1257bp//64%//AF169797

C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.10E-214//1026bp//97%//X96484

C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds//0//1669bp//88%//U49055

C-NT2RP2006241//H.sapiens

300aa//32%//P4466

C-NT2RP2006312//Homo sapiens BAF101 (BAF57) gene, complete cds//2.80E-274//1236bp//99%//AF035262

C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX)//

3.40E-07//50aa//50%//Q61658

C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LGI1) mRNA, complete cds.//1.30E-37//484bp//65%//AF055636

C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266

5 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131

C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//3.10E-272//1220bp//95%//AF038966

10 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE).//4.20E-134//486aa//50%//P24461

C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543

C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538

15 C-NT2RP3000031//HISTONE DEACETYLASE HDA1.//1.10E-71//350aa//42%//P53973

C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559

C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755

C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa//53%//Q05481

20 C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1).//2.20E-06//165aa//27%//Q62245

C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN[CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.90E-123//436aa//50%//P46401

25 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692

C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%//P08640

C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-84//453aa//42%//Q04652

C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334

30 C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, pi 30, complete cds.//0//2730bp//82%//D29766

C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978

C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135

35 C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%//AF106622

C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%//AF120334

C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760

40 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219

C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%//P35293

C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266//1373bp//86%//AF061817

45 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1.70E-139//679aa//41%//O43143

C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185

C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-15//319aa//26%//P37908

50 C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//3.40E-42//645bp//67%//AF098066

C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667

C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%//P28160

C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//200%//P33099

C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%//P35843



C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.//0//3606bp//99%//AF198358

C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.30E-99//669bp//83 %//Y18101

5 C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds.//4.20E-29//530bp//63%//AB017594

C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.40E-16//175aa//28%//P51508

C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.60E-25//129aa//34%//P32089

10 C-NT2RP3001383//Mus musculus ARL-6 interacting protein-6 (Aip-6) mRNA, partial cds.//3.40E-40//355bp//79%//AF133913

C-NT2RP3001384//Homo sapiens mRNA for LA95 protein.//0//1214bp//99%//AJ243467

C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.30E-61//374aa//36%//P49711

C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538

15 C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009

C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1.00E-16//77aa//46%//O33529

C-NT2RP3001427//WERNER SYNDROME HEUCASE HOMOLOG.//2.70E-10//159aa//33%//O09053

C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.40E-128//152aa//99%//P 12270

C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2).//3.20E-90//157aa//59%//P36371

20 C-NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.//4.60E-20//792bp//59%//AF205831

C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.10E-13//87aa//43%//P11632

C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395

C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801

25 C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds.//4.30E-290//793bp//93%//U63420

C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1.00E-61//345aa//42%//P20964

C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//9.10E-10//158aa//31%//Q10022

30 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//388aa//32%//P46821

C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//0//1730bp//85%//AF163665

C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//2617bp//99%//U35832

35 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.80E-18//91aa//38%//Q92609

C-NT2RP3001646//WD-40 REPEAT PROTEIN MS12.//8.80E-09//132aa//31%//O22468

C-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1557bp//98%//AJ012449

C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds.//0//2836bp//99%//AF149046

40 C-NT2RP3001679//Homo sapiens rec mRNA, complete cds.//0//2495bp//99%//AB023584

C-NT2RP3001688//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1869bp//99%//AF173868

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//P25386

45 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.40E-33//161aa//32%//P54356

C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534

C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//1138bp//63%//AF193613

50 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177

C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554

C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT) //7.10E-132//294aa//84%//Q14141

C-NT2RP3001742//HUMAN ENDOGENOUS NUCLEAR RIBONUCLEOPROTEIN M1 (HNRNP M1) //1.80E-117//462aa//55%//P52272

- C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE//1.60E-11//348aa//27%/P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN)//7.40E-18//249aa//30%/Q04652  
 C-NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds//0//2742bp//99%/AF155135
- 5 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1)//8.10E-125//302aa//60%/P55347  
 C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.20E-14//242aa//24%/Q00808  
 C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds//0//1587bp//100%/AB000624
- 10 C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds//4.30E-91//656bp//81%/AF177478  
 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-)//1.30E-22//227aa//33%/P08458  
 C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III//3.10E-92//314aa//51%/Q09251
- 15 C-NT2RP3001969//TRICHOHYALIN//2.70E-11//442aa//23%/P37709  
 C-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.50E-192//475bp//94%/X86779  
 C-NT2RP3002007//SAP1 PROTEIN//1.1 OE-68//474aa//32%/P39955  
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III//5.30E-25//139aa//48%/Q09232
- 20 C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT//1.00E-299//397aa//94%/P18484  
 C-NT2HP3002056//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1)//2.00E-48//475aa//35%/P29374  
 C-NT2RP3002062//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds//0//3764bp//99%/AF095195
- 25 C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds//4.10E-233//1896bp//69%/AF111423  
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN)//7.90E-09//181aa//22%/Q12387  
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS)//2.80E-253//474aa//93%/P15170
- 30 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP//1.90E-151//223aa//91%/Q02614  
 C-NT2RP3002273//SCD6 PROTEIN//1.30E-09//295aa//28%/P45978  
 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE)//8.60E-49//243aa//43%/Q58767
- 35 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds//0//2443bp//99%/U87791  
 C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15)//4.20E-70//590bp//76%/X16396  
 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21)//8.60E-79//416aa//34%/P33991
- 40 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE)//3.70E-43//318aa//37%/P05792  
 C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS45//8.90E-95//542aa//38%/P38932  
 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III//5.80E-40//161aa//52%/Q10010
- 45 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2)//2.90E-19//173aa//28%/P11598  
 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//2.50E-26//90aa//42%/P38660
- 50 C-NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds//0//1703bp//99%/AF111109  
 C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds//0//2109bp//87%/AF165163  
 C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds//8.10E-263//1243bp//97%/AF103731
- C-NT2RP3002664//Homo sapiens putative glycolipid transfer protein mRNA, complete cds//8.10E-263//1243bp//97%/AF103731  
 C-NT2RP3002682//Homo sapiens putative glycolipid transfer protein mRNA, complete cds//0//1596bp//98%/AF111190  
 C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif11b), complete cds//1.10E-93//1205bp//69%/D17577  
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116//1.00E-07//70aa//

41%/P17564

C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%/Q24371

C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%/Q31125

C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%/P51026

C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%/AF030430

C-NT2RP3002876//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.30E-29//805bp//61%/AF053091

C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP).//1.50E-125//512aa//47%/Q13625

C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2.00E-111//551aa//42%/Q04652

C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%/AF152498

C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%/D89053

C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%/AB029333

C-NT2RP3002988//Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds.//1.80E-292//1325bp//99%/AF080158

C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%/AF084555

C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//82%/U78090

C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%/Q02357

C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%/P23645

C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds.//2.60E-112//633bp//88%/AB027149

C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.60E-83//807bp//72%/D88315

C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//91%/AB011414

C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%/AF071592

C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%/AF077738

C-NT2RP3003185//TROPOMYOSIN1, FUSION PROTEIN 33.//2.80E-06//402aa//23%/P49455

C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.30E-98//269aa//62%/P52742

C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa//31%/Q09674

C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851 bp//76%/AF110267

C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%/U20286

C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%/AB030656

C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%/AF098462

C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-86//366aa//48%/P19474

C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%/L36983

C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5e-310//1468bp//82%/AB033922

C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%/O64948

C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.//0//2476bp//99%/AF117657

C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))

C-NT2RP3003353//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%/U09874

- C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
- C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317
- 5 C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds.//4.50E-81//649bp//67%//AB019435
- C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.60E-36//842bp//62%//AF091624
- C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009
- 10 C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%//P40529
- C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//AF106681
- C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- 15 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885
- C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209
- C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
- C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
- 20 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//U28164
- C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294
- C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457
- 25 C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
- C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
- C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
- 30 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//AB019435
- C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//4.50E-147//874bp//87%//U19181
- C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
- 35 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//AF086628
- C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692
- C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
- 40 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091
- C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747
- C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
- 45 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
- C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
- C-NT2RP3004206//CROOKED NECK PROTEIN.//1.40E-220//567aa//67%//P17886
- C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820
- 50 C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0//2320bp//99%//AF126736
- C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%//P52734
- C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0//1861bp//99%//AF065391
- C-NT2RP3004282//Homo sapiens torsinA (p11) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871
- C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//

X67877

C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds//3.90E-38//462bp//70%/AF225902

C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%/AJ007798

5 C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KD PROTEIN) (MI2-BETA).//5.20E-09//212aa//25%/Q14839

C-NT2RP3004472//GERM CELL-LESS PROTEIN//1.60E-61//170aa//40%/Q01820

C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.30E-113//466aa//42%/P34110

10 C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//4.00E-303//1385bp//99%/AB012851

C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.00E-249//1777bp//80%/U83176

C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%/Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%/P40484

15 C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0//2075bp//87%/L11316

C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//1.3aa//53%/Q15642

C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%/P51523

20 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//150aa//28%/Q01484

C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//0//1853bp//99%/AF040701

C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%/P39922

25 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%/AJ006266

C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%/Q02084

C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%/AF093097

30 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa//45%/P54352

C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//0//2393bp//99%/AB014679

C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%/P35526

C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%/Q64375

35 C-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//2160bp//99%/AJ012449

C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%/AB011538

C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%/Q10568

40 C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.//1.40E-28//296bp//75%/AF176667

C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//4.30E-188//1543bp//78%/U35776

C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%/P22579

45 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%/P15287

C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%/AJ006470

C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%/Q03173

C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.50E-29//153aa//43%/O23968

50 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1.//3.50E-297//1024aa//55%/P87115

C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.50E-26//237aa//28%/Q01631

C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//32%/P26372

C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) //2.60E-77//262aa//54%/O75570

C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) //2.60E-77//262aa//54%/O75570

C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243  
 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.90E-110//435aa//50%//P52738  
 C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds.//6.20E-19//902bp//57%//AF221546  
 5 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE)(FRAGMENT).//2.60E-51//438aa//33%//P45701  
 C-NT2RP4000449//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3143bp//99%//AF083106  
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.00E-07//175aa//27%//P09309  
 10 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//2.50E-37//291aa//38%//P50101  
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.90E-67//721aa//29%//Q09475  
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.80E-50//214aa//50%//P40484  
 15 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.50E-106//495aa//45%//P45818  
 C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds.//0//3131bp//87%//AF022962  
 C-NT2RP4000528//NPL4 PROTEIN.//9.80E-86//515aa//37%//P33755  
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.40E-14//233aa//31%//P40319  
 20 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.90E-188//863bp//99%//AF067730  
 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.70E-07//175aa//27%//P09309  
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.10E-32//350aa//30%//P39625  
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.10E-13//295aa//27%//Q11073  
 25 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.20E-191//199aa//78%//P10267  
 C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.//4.60E-250//1462bp//84%//AF176524  
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000032//67aa//31%//P53915  
 30 C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.80E-11//503aa//23%//P08640  
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.30E-94//810bp//65%//Y18265  
 C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.50E-21//271aa//28%//Q00808  
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.70E-82//324aa//48%//O09175  
 35 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.10E-85//174aa//55%//P16415  
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.20E-91//173aa//87%//O35682  
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME EI (A1S9 PROTEIN).//9.60E-96//513aa//42%//P22314  
 C-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//0//2127bp//86%//D45913  
 40 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.60E-26//227aa//36%//Q06828  
 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.50E-76//346aa//43%//Q61068  
 45 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521  
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HEUCASE MJ1505.//1.40E-07//185aa//25%//Q58900  
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.40E-26//90aa//42%//P38660  
 50 C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.//2.30E-81//389bp//100%//AF094583  
 C-NT2RP4000989//UNC-47 PROTEIN.//8.20E-06//173aa//25%//P34579  
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700  
 C-NT2RP4001011//Rattus norvegicus 8D-95 SAP90-associated protein mRNA, complete cds.//0//377bp//91%//U067140  
 C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//

AF198487

C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.50E-92//443aa//44%/Q09996

C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65//6.70E-51//335aa//37%/Q64375

5 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE)//1.30E-123//563aa//46%/P13586

C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds//0//1439bp//99%/AB023967

C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//2.30E-07//474aa//22%/P12036

10 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1)//2.60E-17//121aa//36%/P51400

C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.90E-115//224aa//100%/P38378

C-NT2RP4001122//mPD PROTEIN//1.40E-65//253aa//741%/O15736

15 C-NT2RP4001126//TRICHOHYALIN//2.90E-18//380aa//26%/Q07283

C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP)//2.10E-07//93aa//33%/P44514

C-NT2RP4001148//SOF1 PROTEIN//1.30E-104//236aa//52%/P33750

20 C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds//4.40E-187//731bp//100%/AF037339

C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO)//3.40E-29//385aa//29%/P35331

C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//4.70E-29//227aa//35%/P52178

25 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds//4.40E-104//1460bp//65%/U95760

C-NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds//0//2940bp//99%/AF111109

C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT)//5.70E-141//511aa//43%/Q99676

30 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)//6.20E-27//90aa//42%/P38660

C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)//1.80E-103//508aa//43%/Q04652

C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein (76p gene)//0//2006bp//100%/AJ249677

35 C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds//0//1866bp//100%/AF174601

C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds//4.40E-58//1196bp//61%/U49082

C-NT2RP4001276//TRICHOHYALIN//7.90E-09//126aa//32%/Q07283

C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSCASE OF OUTER MEMBRANE 40 KD SUBUNIT)//5.90E-17//296aa//29%/P24391

40 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5//8.50E-213//1129bp//92%/AJ001119

C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN//0.000016//186aa//29%/O24076

C-NT2RP4001339//Homo sapiens mRNA for AMMER1 protein//9.20E-160//736bp//99%/AJ007014

45 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds//2.7E-310//1400bp//100%/AB017494

C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//1.40E-58//2425bp//59%/U53445

50 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//1.60E-19//222aa//30%/Q08180

C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1)//9.20E-17//146aa//35%/P18160

C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I//2.00E-53//436aa//30%/Q10085

C-NT2RP4001414//TRICHOHYALIN//1.40E-05//298aa//21%/P22790

C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//7.70E-190//422aa//82%/Q14141

C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.20E-138//419aa//54%/Q99676

- C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds//2.70E-66//738bp//71%//AF129131
- C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE)//0//962aa//78%//Q02218
- 5 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1//1.00E-27//374aa//29%//P39010
- C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds//0//2002bp//98%//AF198487
- C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION//5.70E-54//242aa//38%//P25656
- 10 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds//0//3202bp//99%//AF152961
- C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-)//4.70E-09//216aa//24%//P96902
- C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN//5.40E-07//213aa//26%//Q02453
- C-NT2RP4001568//ZINC FINGER PROTEIN GCS1//1.80E-10//109aa//36%//P35197
- 15 C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//0//874aa//96%//P53620
- C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein//0//1087bp//87%//AJ223830
- C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//1.70E-141//373aa//47%//P73505
- 20 C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//2.80E-14//652aa//22%//Q02224
- C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19//5.10E-46//234aa//32%//P40469
- C-NT2RP4001644//MYOSIN UGHT CHAIN KINASE (EC 2.7.1.117) (MLCK)//6.40E-19//111aa//45%//P25323
- C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN)//1.10E-45//310aa//27%//P12868
- 25 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//4.00E-10//243aa//25%//Q10568
- C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//3.00E-10//128aa//32%//Q10282
- 30 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT)//6.40E-170//1168aa//33%//Q09332
- C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//3.90E-236//665aa//58%//P51523
- C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN)//4.10E-16//263aa//27%//P98174
- 35 C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds//0//3053bp//99%//AF170025
- C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)//1.20E-30//241aa//30%//Q03566
- 40 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4//1.10E-19//77aa//54%//P55083
- C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds//6.30E-99//555bp//73%//AF155595
- C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1//1.40E-85//489aa//43%//P55194
- C-NT2RP4001861//HTUCHOHYALIN//1.00E-35//307aa//34%//P37709
- 45 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.40E-08//345aa//25%//Q00808
- C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1//1.30E-38//258aa//32%//Q12024
- C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF//9.80E-60//303aa//38%//P49711
- C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL METHYLTRANSFERASE)//1.50E-13//211aa//28%//Q43209
- 50 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//1.20E-13//356aa//27%//P13816
- C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds//0//3203bp//87%//AF195418
- C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds//0//3024bp//99%//AF236056
- C-NT2RP4002047//GTP-BINDING PROTEIN PPA//1.1E-168//601aa//52%//Q67614
- C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.00E-137//679aa//40%//Q43143

C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//3.00E-150//722aa//39%/Q05481  
 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND PI 9 SUBUNITS) (TFIIA-42) (TFIIAL)//6.70E-06//250aa//31%/P52655  
 5 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-)//1.50E-63//159aa//53%/P38938  
 C-NT2RP4002791//NUCLEOPROTEIN TPR//6.50E-05//659aa//23%/P12270  
 C-NT2RP5003461//RLR1 PROTEIN//9.70E-22//177aa//27%/P53552  
 C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//5.50E-15//280aa//27%/Q00808  
 10 C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds//1.30E-237//820bp//87%/AB024565  
 C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RALG1) mRNA, complete cds//0//2289bp//99%/AF095448  
 C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)//3.30E-23//219aa//40%/P37116  
 15 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds//7.00E-217//683bp//99%/AB029290  
 C-OVARC1000006//HISTONE H2A.1//1.10E-55//117aa//99%/P02262  
 C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1)//4.20E-06//102aa//32%/O14727  
 20 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//2.60E-295//1393bp//97%/AF058922  
 C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE)//3.20E-07//60aa//45%/P80022  
 C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds//1.50E-47//727bp//67%/AF156957  
 25 C-OVARC1000085//Human mRNA for proteasome subunit HC5//1.00E-151//699bp//100%/D00761  
 C-OVARC1000087//HISTONE MACRO-H2A.1//1.60E-12//174aa//26%/Q02874  
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF)//8.40E-14//259aa//30%/P51610  
 C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33//0.000032//165aa//27%/P49455  
 30 C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG)//2.70E-12//120aa//32%/Q13107  
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl//2.50E-95//461bp//98%/AJ242975  
 35 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds//1.80E-32//511bp//65%/AF068332  
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA)//8.20E-120//351aa//54%/Q16665  
 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI)//5.40E-53//384aa//30%/P14904  
 40 C-OVARC1000304//PROTEIN MOV-10//1.10E-249//519aa//87%/P23249  
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2)//2.70E-40//154aa//38%/P29363  
 C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds//9.20E-148//787bp//76%/U19614  
 45 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION//5.90E-14//200aa//27%/P40004  
 C-OVARC1000437//TENSIN//7.90E-181//340aa//84%/Q04205  
 C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7//1.20E-25//227aa//25%/P11075  
 50 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR)//3.10E-10//125aa//35%/P51452  
 C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds//0//1872bp//89%/D87671  
 C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//2.20E-157//892bp//91%/AF051850  
 C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.1) (S6KII ALPHA 2) (PDC DOK 1)  
 C-OVARC1000564//Homo sapiens protein tyrosine kinase 5 (LAX5) mRNA, complete cds//0//1218bp//91%/U121855  
 C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-

plete cds.//0//1812bp//98%//D43772

C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888

C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.10E-209//293aa//95%//P39098

5 C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//0//759bp//98%//AF038661

C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN//0.00000017//78aa//48%//P25159

C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C)//5.60E-11//74aa//37%//P49596

10 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%//P08886

C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75)//3.90E-46//78aa//98%//O35501

C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp//99%//Y17711

C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199

15 C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0//2095bp//99%//AF045584

C-OVARC1000862//M.musculus mRNA for FT1.//5.90E-226//1498bp//81%//Z67963

C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.20E-50//206aa//52%//P40484

C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440

20 C-OVARC1000915//Homo sapiens histone deacetylase 5 mRNA, complete cds.//1.60E-121//591bp//97%//AF132608

C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398

C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aabbp//49%//P32943

C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//82%//AB005549

25 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.20E-17//127aa//33%//Q58343

C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527

C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.50E-178//1113bp//86%//AF001533

C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978

30 C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566

C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSORS.//1.90E-35//76aa//98%//P43490

C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1.00E-215//1027bp//98%//AF132946

C-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//0//1819bp//99%//AF082657

35 C-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//2.00E-214//769bp//97%//AJ005897

C-OVARC1001107//Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.//6.10E-276//594bp//98%//AF167572

40 C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//AF051782

C-OVARC1001154//Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.//2.30E-296//1561bp//93%//AF055008

C-OVARC1001171//Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.//5.70E-151//436bp//92%//U94855

45 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.10E-11//221aa//25%//P48510

C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192

C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//5.10E-22//83aa//37%//Q10568

50 C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//X62083

C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//224aa//26%//P25976

C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444

C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058

C-OVARC1001391//Homo sapiens mRNA for candidate tumor suppressor involved in B cell development.//0//1467bp//99%//AJ224819

C-OVARC1001417//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170

mRNA, complete cds.//0//1715bp//99%//AF135802

C-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.90E-48//586bp//69%//U52426

C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111

C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds.//1.80E-187//510bp//89%//  
5 AB017616

C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//  
AF016507

C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE  
PROTEIN 1)//0//777aa//91%//P98161

10 C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.40E-19//130aa//40%//P53081

C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//  
AF031165

C-OVARC1001610//Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.//0//  
1870bp//99%//AF068302

15 C-OVARC1001703//Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.//3.50E-16//399bp//  
61%//AF133670

C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B)//2.80E-10//106aa//  
38%//Q62267

C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-  
AZEPAM BINDING INHIBITOR) (MA-DBI).//4.40E-40//195aa//41%//P07106

C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%//Q13796

C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//262aa//65%//  
P08942

25 C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
NO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%//P12945

C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//  
0//963bp//99%//U97670

C-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.70E-190//1624bp//76%//  
AF068748

30 C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
NO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%//P12945

C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds.//0//2035bp//87%//AF143859

C-OVARC1001987//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//  
0//1083bp//99%//AF203687

35 C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%//  
AB029290

C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%//Q02874

C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-  
ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%//  
40 Q035913

C-OVARC1002138//SAP1 PROTEIN.//7.60E-60//128aa//59%//P39955

C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%//AF195851

C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-  
REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213

45 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-  
09//207aa//30%//Q91854

C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%//AB019602

C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
(UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
ZYME).//1.60E-81//212aa//70%//P34547

50 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%//P08643

C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%//L22154

C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%//P53538

C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U163127

C-PLACE1000082//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U163127

C-PLACE1000083//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U163127

C-PLACE1000084//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U163127

C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29//  
134aa//43%//P52046

C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%//AF058291

C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase.//4.90E-258//1183bp//99%//AJ242910

C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//4.50E-05//197aa//26%//P08640

C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979

C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%//P15151

C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//334aa//72%//P23246

C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//2.80E-06//134aa//29%//P53368

C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//U35245

C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421

C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522

C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%//P32455

C-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1540bp//99%//AJ012449

C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918

C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.00E-55//779bp//67%//AF044201

C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.20E-39//261aa//27%//Q08891

C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1992bp//99%//AF180371

C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLC110F1857Q7 (RZPD Berlin)).//2.10E-277//1260bp//99%//AJ005896

C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//0//1366bp//99%//AF119043

C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.60E-250//1189bp//97%//AB028449

C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.//0//1985bp//98%//AF132952

C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734

C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645

C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.50E-49//181aa//54%//P32899

C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.60E-19//404aa//26%//P39010

C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.40E-22//129aa//35%//Q03070

C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742

C-PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.//5.90E-278//1476bp//92%//AF110195

C-PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.//0//1988bp//99%//AJ131721

C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//1355bp//100%//AB024301

C-PLACE1001062//Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS.//1.60E-207//742bp//99%//AJ007714

C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485

C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//6.80E-18//529aa//23%//Q99323

C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742

C-PLACE1001171//MYOTUBULARIN.//7.10E-84//198aa//73%//Q13496

C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.00E-202//1333bp//80%//D14336

AF058291

AF058291 Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%//AF058291

C-PLACE1001304//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//0//2145bp//

99%//AF159567

C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//AF009615

C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIREMENT).//3.00E-33//138aa//42%//Q61103

C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.30E-61//132aa//46%//Q12929

C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.//4.60E-112//392bp//87%//AB002137

C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.70E-130//244aa//99%//Q60809

C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-118//429aa//48%//P51523

C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.30E-66//174aa//45%//P91408

C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4.00E-81//263aa//56%//P08635

C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.50E-75//439aa//41%//P16381

C-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//2602bp//99%//AF061243

C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%//AJ006276

C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.40E-63//427aa//35%//Q57290

C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953

C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%//AF159159

C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2.00E-27//270aa//31%//P94524

C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935

C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%//P37908

C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091

C-PLACE1002046//UGATIN (FRAGMENT).//1.70E-240//560aa//80%//Q61211

C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.30E-07//188aa//29%//P49606

C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.50E-58//112aa//100%//O76094

C-PLACE1002140//Rattus norvegicus apelin mRNA, complete cds.//1.40E-43//425bp//74%//AF179679

C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591

C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.90E-100//966bp//75%//AB030505

C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.10E-05//278aa//24%//P50533

C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233

C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//4.20E-06//133aa//29%//Q13105

C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274

C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262

C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.70E-113//545bp//98%//AF042273

C-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%//U50927

C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.20E-152//289aa//96%//P70396

C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99//386aa//48%//P45890

C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).//5.60E-34//76aa//98%//P39087

C-PLACE1002591//CORONIN-UKE PROTEIN P57.//4.40E-70//208aa//66%//P31146

C-PLACE1002654//ADSEVERIN (ADSEVERIN).//3.50E-278//543aa//92%//Q28047

C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765

C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//0//1750bp//99%//AF068180

C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)//9.40E-13//500aa//21%//Q99323

5 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001//9.00E-45//305aa//33%//Q15391

C-PLACE1002775//PEREGRIN (BR140 PROTEIN)//3.80E-13//272aa//28%//P55201

C-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds//3.80E-43//385bp//77%//U50927

10 C-PLACE1002816//HISTONE DEACETYLASE HDA1//2.20E-48//217aa//46%//P53973

C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//5.50E-203//396aa//86%//P51522

C-PLACE1002908//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds//0//1654bp//99%//AB028600

15 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4)//1.40E-78//496aa//37%//Q49091

C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//8.50E-44//225bp//100%//AF032387

C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTIN) (R48321)//1.70E-05//150aa//24%//Q13563

20 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D)//2.60E-79//253aa//60%//Q13268

C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)//3.80E-37//143aa//51%//P42743

C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl-DNA phosphodiesterase protein (TDP1) mRNA, partial cds//1.70E-148//687bp//99%//AF182003

25 C-PLACE1003190//SOF1 PROTEIN//1.90E-110//325aa//48%//P33750

C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001//4.90E-76//309aa//47%//Q15391

C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN//7.90E-22//70aa//47%//P21541

C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//6.90E-206//396aa//86%//P51522

30 C-PLACE10033537//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//0//2435bp//99%//U92715

C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds//1.40E-78//542bp//67%//AF107403

C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds//2.60E-139//648bp//99%//AF152463

35 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W//1.30E-40//278aa//36%//P40556

C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR//1.70E-23//322aa//26%//Q13201

C-PLACE1003519//H.sapiens hnRNP-E2 mRNA//5.10E-218//905bp//99%//X78136

C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//0.0000011//101aa//32%//Q09475

40 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT)//7.70E-68//404aa//33%//P32802

C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG//2.60E-93//270aa//66%//P46975

45 C-PLACE1003602//Homo sapiens mRNA expressed in placenta//5.90E-278//1275bp//99%//D83200

C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR//0.00000023//82aa//35%//Q02516

C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds//6.20E-169//683bp//99%//AF191338

50 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN//3.20E-10//380aa//25%//P18824

C-PLACE1003669//TRICHOHYALIN//5.60E-09//219aa//30%//P22793

C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//8.00E-19//209aa//34%//Q08170

C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA complete cds//6.20E-282//1313bp//99%//AF133423

C-PLACE1003766//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) mRNA, complete cds//5.20E-289//1313bp//99%//AF133423



C-PLACE1004814//SPlicing FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPlicing FACTOR SRP75)//5.90E-19//196aa//36%//Q08170  
 C-PLACE1004868//MALE STERILITY PROTEIN 27//3.90E-39//261aa//27%//Q08891  
 C-PLACE1004902//PUTATIVE PRE-MRNA SPlicing FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C//9.30E-11//94aa//47%//O42643  
 5 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A)//4.90E-48//198aa//44%//P06151  
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936  
 C-PLACE1004937//SEL-10 PROTEIN//6.30E-125//357aa//58%//Q93794  
 10 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X//2.00E-14//205aa//26%//Q11073  
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds//6.6e-313//1413bp//99%//AF132950  
 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN)//2.60E-56//565aa//30%//Q04652  
 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds//3.90E-212//1040bp//96%//AF113539  
 15 C-PLACE1005187//APAG PROTEIN//3.80E-13//122aa//36%//P05636  
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-)//1.30E-27//349aa//32%//Q01577  
 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP)//2.30E-13//269aa//28%//P53352  
 20 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//2.00E-111//226aa//92%//P08760  
 C-PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds//1.20E-226//748bp//95%//AF209931  
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)//8.60E-09//194aa//27%//O33335  
 25 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A)//1.10E-09//93aa//31%//P32959  
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6//0//1649bp//99%//AJ006276  
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III//5.60E-52//173aa//57%//Q09251  
 30 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A//7.60E-97//1287bp//67%//AJ010046  
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27//1.90E-11//60aa//48%//P46288  
 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPQ (P135 PROTEIN) (IER 2.9/ER2.6)//6.80E-09//267aa//30%//P29128  
 35 C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds//2.00E-33//379bp//66%//AB028860  
 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//0//2130bp//99%//AF083255  
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE)//2.10E-148//321aa//83%//P31350  
 40 C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds//2.00E-118//378bp//98%//AF162680  
 C-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11//1.30E-237//585aa//72%//Q60710  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II)//2.50E-79//209aa//53%//P08635  
 45 C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene)//0//1985bp//99%//AJ275986  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//1.10E-217//994bp//99%//AF027156  
 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//0//2040bp//99%//AF065482  
 50 C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//0//730aa//99%//Q10568  
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT)//9.90E-42//224aa//43%//P54069  
 C-PLACE1005921//AIG1 PROTEIN//3.00E-31//284aa//31%//P54120  
 C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PRFB) mRNA, complete cds//0//2641bp//99%//AF026681  
 C-PLACE1005953//GLUTAMATE TRANSFERASE ACIDIC//0//198aa//97%//P43639  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.40E-54//455aa//32%//P14904

C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)/71.40E-07//254aa//25%/P38129  
C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%/AF151852  
C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%/AJ236876  
C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.70E-161//744bp//99%/X99906  
C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.50E-148//681bp//99%/AF039023  
C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2.00E-28//236aa//30%/P98110  
C-PLACE1006167//PAF1 PROTEIN.//7.30E-15//437aa//24%/P38351  
C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.70E-169//373aa//88%/P17427  
C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.70E-116//496aa//48%/Q09747  
C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2.00E-16//244aa//31%/P28675  
C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//4.60E-117//147aa//80%/P21796  
C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%/U76374  
C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//0//1649bp//99%/AF155112  
C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//1.30E-18//460aa//24%/Q00547  
C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%/AF062085  
C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.50E-45//122aa//43%/P49910  
C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.20E-83//313aa//49%/P27550  
C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.70E-55//142aa//85%/Q90595  
C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.10E-229//367aa//96%/Q00004  
C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds.//0//2618bp//99%/AF137030  
C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//2170bp//99%/AF191338  
C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//1967bp//99%/AF093097  
C-PLACE1006534//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)(PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAM-INYLTRANSFERASE) (GALNAC-T1).//8.30E-08//100aa//41%/Q10472  
C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.20E-09//426aa//21%/P39922  
C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//0//1464bp//99%/U97670  
C-PLACE1006626//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.90E-13//177aa//33%/Q59263  
C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//6.20E-63//191aa//43%/P13688  
C-PLACE1006819//UNE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.80E-213//232aa//80%/P08547  
C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE- RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI- TOUS NUCLEAR PROTEIN) //2.00E-15//188aa//29%/P35123  
C-PLACE1006851//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006852//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006853//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006854//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006855//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006856//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006857//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006858//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006859//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006860//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006861//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006862//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006863//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006864//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006865//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006866//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006867//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006868//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006869//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006870//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006871//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006872//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006873//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006874//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006875//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006876//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006877//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006878//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006879//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006880//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006881//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006882//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006883//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006884//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006885//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006886//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006887//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%/AB028449  
C-PLACE1006888//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%/AB015630  
C-PLACE1006889//

Q10000

C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1 //1.30E-86//522aa//36%//P97998

C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421

5 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.20E-35//180aa//33%//Q14542

C-PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.//0//2449bp//98%//AF047489

C-PLACE1007140//TRICHOHYALIN//1.30E-25//816aa//22%//P37709

10 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.1.1.1) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa//31%//P54304

C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.50E-216//1068bp//96%//D50495

C-PLACE1007243//UNC-47 PROTEIN.//1.70E-07//211aa//27%//P34579

C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908

15 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.10E-17//1037bp//56%//AF117649

C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870

20 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715

C-PLACE1007409//WHITTE PROTEIN.//1.10E-64//428aa//32%//Q17320

C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.80E-25//140aa//35%//P27487

25 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.40E-53//426aa//33%//P52734

C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.40E-85//385aa//45%//P08728

C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164

30 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.00E-49//361aa//36%//P34537

C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.60E-143//666aa//44%//Q99676

C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//1.00E-07//228aa//31%//P32506

35 C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640

C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.70E-09//279aa//28%//Q26457

C-PLACE1007697//GCN20 PROTEIN.//7.60E-119//717aa//38%//P43535

40 C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%//AB033922

C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243

C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.50E-44//231aa//42%//P10265

C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602

C-PLACE1007897//Homo sapiens FLASH mRNA, complete cds.//0//2145bp//99%//AF154415

45 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.60E-14//370aa//25%//Q99323

C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//6.70E-13//168aa//31%//P38226

50 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530

C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529

C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa//48%//P52272

C-PLACE1008000//HOMO SAPIENS CYCLIN D BINDING PROTEIN mRNA

C-PLACE1008001//HOMO SAPIENS CYCLIN D BINDING PROTEIN mRNA

C-PLACE1008002//HOMO SAPIENS CYCLIN D BINDING PROTEIN mRNA

C-PLACE1008003//HOMO SAPIENS CYCLIN D BINDING PROTEIN mRNA

- C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179
- C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.)//3.00E-25//208aa//37%//Q03326
- C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//31%//Q09531
- 5 C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%//P37709
- C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077
- C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808
- C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//671aa//77%//P53620
- 10 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%//P12689
- C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//77%//AF078779
- C-PLACE1008330//EOSINOPHIL LYOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%//Q05315
- 15 C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//7.1.90E-170//780bp//100%//AF036144
- C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%//Q04652
- C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432
- C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRAN-SCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541
- 20 C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//1.80E-11//365aa//25%//O42184
- C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%//Q06527
- C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%//AJ277275
- 25 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//48%//P22620
- C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.80E-236//453aa//96%//P37199
- C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
- 30 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN H2).//5.20E-90//483aa//38%//O02668
- C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%//O13615
- C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF03 8406
- 35 C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0//1670bp//99%//AF060543
- C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.30E-269//1225bp//99%//AJ004974
- C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%//AF032668
- C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%//P12623
- 40 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112
- C-PLACE1009060//BRO1 PROTEIN.//6.70E-19//567aa//24%//P48582
- C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//30%//P30432
- C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%//P51814
- 45 C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586
- C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2.00E-68//181aa//43%//Q05086
- C-PLACE1009158//Mus musculus mRNA for death inducer-oblierator-1 (Dio-1).//5.40E-200//1790bp//75%//AJ238332
- 50 C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255//1179bp//98%//AF150105
- C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675
- C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%//P1492
- C-PLACE1009308//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432
- C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds, nuclear gene for mitochondrial product.//2.10E-132//1229bp//75%//AF107295

C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX27/2.50E-10//151aa//29%/Q12067  
 C-PLACE1009398//ZINC FINGER PROTEIN 135//6.20E-97//361aa//51%/P52742  
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I//4.70E-08//165aa//33%/Q09820  
 5 C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds//1.00E-173//1367bp//77%/AF176523  
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA)//7.80E-71//82aa//89%/P42356  
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)//3.10E-289//550aa//93%/P54319  
 10 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III//3.90E-40//179aa//37%/P34580  
 C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds//6.60E-147//592bp//99%/AF043117  
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR) 7/8.10E-99//228aa//75%/Q99418  
 15 C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds//5.90E-185//857bp//99%/AF078857  
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//5.10E-54//291aa//40%/Q00808  
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN//1.30E-60//209aa//41%/P25159  
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN)//1.50E-285//538aa//99%/P55161  
 20 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//0//1854bp//100%/AF062534  
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I//7.00E-33//166aa//43%/Q09876  
 C-PLACE1009721//MSF1 PROTEIN//1.70E-22//176aa//33%/P35200  
 25 C-PLACE1009731//AIG1 PROTEIN//1.60E-22//274aa//28%/P54120  
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds//4.30E-294//1329bp//100%/AB012190  
 C-PLACE1009798//RLR1 PROTEIN//1.60E-18//270aa//23%/P53552  
 C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31)//2.30E-59//405aa//33%/P38968  
 30 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-)//6.50E-28//209aa//38%/P43510  
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION//1.90E-108//277aa//43%/P53145  
 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds//0//1730bp//99%/AF038963  
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84)//4.60E-59//450aa//34%/P28175  
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds//5.20E-70//736bp//73%/U48288  
 40 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein//6.00E-279//1402bp//94%/X84692  
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//0//2019bp//99%/AF065482  
 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-)//1.40E-268//506aa//98%/Q62671  
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN)//7.30E-114//537aa//44%/Q04652  
 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3)//1.70E-20//156aa//42%/P22082  
 45 C-PLACE1010148//CYUCIN I (MULTIPLE-BAND POLYPEPTIDE I)//4.60E-07//431aa//23%/P35662  
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//9.80E-11//95aa//49%/Q01130  
 50 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)//5.10E-27//371aa//28%/Q14246  
 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN//1.60E-77//214aa//62%/P25722  
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//1.20E-18//467aa//30%/P46804  
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)

C-PLACE1010382//PHOSPHATIDYLINOSITOL 3-OH PHOSPHATASE (PI-PLC) PRECURSOR  
 PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)//2.00E-09//126aa//29%/P34024  
 C-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds//0//2082bp//91%/AF003927

- C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981 bp//99%//AB022718
- C-PLACE1010529//Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.//0//1750bp//99%//AF191838
- 5 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//1.20E-07//616aa//24%//P25386
- C-PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.//8.80E-300//1359bp//99%//AF191771
- 10 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546
- C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642
- C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
- C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS 13.//5.70E-75//423aa//39%//Q01755
- 15 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332
- C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
- C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4.00E-299//1091bp//99%//AB019987
- 20 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.90E-91//668bp//82%//AF020267
- C-PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.//0//1448bp//99%//AB034205
- C-PLACE1010771//M.musculus HCNGP mRNA.//7.40E-168//966bp//89%//X68061
- 25 C-PLACE1010811//Rattus norvegicus mRNA for protein encoded by bdeight gene, partial.//1.60E-217//858bp//87%//AJ010392
- C-PLACE1010833//CALTRACTIN(CENTRIN).//0.0000001//154aa//28%//P41209
- C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-143//407aa//58%//Q05481
- 30 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580
- C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//7.60E-23//103aa//53%//Q09746
- C-PLACE1010942//Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.//0//1440bp//99%//AF114487
- 35 C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.30E-98//297aa//48%//P45890
- C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019
- C-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//0//646aa//97%//P10894
- 40 C-PLACE1011056//HISTONE HI, GONADAL.//6.80E-13//154aa//37%//P02256
- C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//1.50E-22//63aa//88%//Q07803
- C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.90E-71//190aa//44%//Q03532
- C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
- 45 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.30E-89//167aa//100%//P03830
- C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.20E-12//212aa//29%//Q03326
- C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
- 50 C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
- C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//7.20E-151//697bp//99%//AF102265
- C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380bp//97%//AB019602
- C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) //1.70E-78//383aa//39%//Q61703
- C-PLACE1011433//TRANSCRIPT 10.1A FOR A-FACTOR.//1.00E-10//236aa//25%//P34694
- C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
- C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

4.90E-11//147aa//32%/P52178

C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.//0//1791bp//82%/L11672

C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds//4.10E-259//1538bp//87%/AF177476

C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA, complete cds.//0//1559bp//99%/AF105377

C-PLACE1011664//CROOKED NECK PROTEIN.//1.60E-187//505aa//64%/P17886

C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.30E-255//1179bp//99%/AF095192

C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%/U61969

C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%/P35580

C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//0//2782bp//99%/AF059617

C-PLACE101-2031//Homo sapiens sorting nexin 13 (SNX13) mRNA, partial cds.//0//1701bp//100%/AF121862

C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.60E-42//104aa//49%/Q09475

C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-116//364aa//45%/P42566

C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//2.70E-107//981bp//74%/AF082556

C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%/P10586

C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//6.10E-293//388aa//99%/P38650

C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347.//6.30E-166//656bp//94%/AB015629

C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%/AF027219

C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%/O15736

C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//6.60E-115//226aa//99%/Q01082

C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//6.00E-57//239aa//34%/Q04652

C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%/P23098

C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.//0//1554bp//99%/AF069307

C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%/Q04205

C-PLACE2000373//F-SPONDIN PRECURSOR.//8.60E-16//371aa//28%/P35446

C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.30E-37//90aa//98%/P10586

C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%/P14209

C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%/Q09996

C-PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%/AF062085

C-PLACE2000427//PROBABLE HELICASE MOT1.//1.20E-26//200aa//27%/P32333

C-PLACE2000438//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.10E-86//348aa//41%/Q10472

C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.50E-25//165aa//40%/P33450

C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//6.70E-127//671bp//94%/AF072733

C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1)(FRAGMENT).//3.50E-30//400aa//30%/P11414

C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA complete cds.//0//2253bp//99%/AF033661

C-PLACE3000038//Mus musculus mRNA for a ubiquitin-conjugating enzyme.//1.79E-99//117aa//37%/P33366

C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281aa//22%/P22224

C-PLACE3000145//TENSIN.//1.00E-108//217aa//15%/Q04205

C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084

C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742

5 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020

C-PLACE3000242//Human trophinin mRNA, complete cds.//0//2290bp//99%//U04811

C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995

C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946

10 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23%//P08640

C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//1.00E-54//418aa//38%//P46549

C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//1.80E-141//565bp//98%//AB029290

15 C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//0//3012bp//98%//AF153085

C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580

C-PLACE4000014//X-LINKED HEUCASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100

20 C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281

C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640

25 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//AF146689

C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aapb//88%//AF091234

C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.40E-235//516aa//51%//Q05481

30 C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746

C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254

C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430

35 C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD proteom.//0//5143bp//90%//Z70200

C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201

C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//0//2034bp//89%//AF032667

C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771

40 C-PLACE4000369//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240 mRNA, complete cds.//1.40E-185//1135bp//67%//AF117754

C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576

C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200

45 C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254

C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//7.70E-60//254aa//44%//P13002

C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.40E-191//828aa//48%//P21783

50 C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%//P08640

C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF).//3.30E-70//226aa//52%//P10079

C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.90E-17//201aa//34%//

P49816

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme//0//6340bp//87%//Y17267

C-SKNC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT)//5.50E-35//431aa//29%//O60100

5 C-SKNC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds//0//2384bp//99%//AF047690

C-SKNC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds//1.90E-162//749bp//99%//AF034800

C-SKNC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE)//3.20E-41//87aa//98%//P17655

10 C-SKNC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds//6.10E-190//872bp//99%//AB021663

C-THYRO1000034//TRICHOHYALIN//9.40E-10//176aa//30%//P37709

C-THYRO1000072//MYOSIN UGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]//3.40E-16//201aa//29%//P11799

15 C-THYRO1000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B//2.00E-72//155aa//92%//Q06710

C-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds//0//1737bp//87%//U49055

C-THYRO1000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds//1.10E-159//824bp//95%//U97018

20 C-THYRO1000173//Homo sapiens AP-mu chain family member muB (HSMU1B) mRNA, complete cds//0//1713bp//99%//AF020797

C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//0//2362bp//99%//AJ005698

C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//5.00E-118//239aa//66%//P51523

25 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//0//2161bp//99%//AB016068

C-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds//0//1567bp//99%//AF124145

C-THYRO1000343//ATROPHIN-1 (DENTATORUBRAL-PALUDOLUYSIAN ATROPHY PROTEIN)//4.90E-06//280aa//31%//P54259

30 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN//2.30E-229//237aa//79%//P17563

C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds//1.20E-299//1325bp//99%//AF072864

C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds//0//2092bp//99%//AF156857

C-THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds//1.10E-90//430bp//99%//U67085

35 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds//0//2254bp//100%//AB022663

C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A))//4.20E-98//408aa//42%//P19474

C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds//0//1557bp//91%//AF118566

40 C-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//0//1901bp//99%//AF075587

C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds//0//3080bp//99%//AF140360

45 C-THYRO1000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds//0//2341 bp//99%//AB024313

C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9//0//2001bp//86%//AJ132889

C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds//0//3347bp//99%//AF095195

50 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131)//3.30E-96//335aa//52%//P98171

C-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII)(STY)//1.80E-55//243aa//42%//Q64686

C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds//2.40E-157//1656bp//70%//U37373

C-THYRO1000800

C-THYRO1000800

C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//0//2387bp//99%//AF079529

- C-THYRO11000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//7.50E-57//315aa//43%/P32322
- C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE)//5.00E-83//566aa//37%/P43550
- 5 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)//6.30E-17//143aa//39%/P35132
- C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN UGASE) (UBIQUITIN CARRIER PROTEIN)//5.90E-14//84aa//41%/P52491
- 10 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521//8.40E-12//167aa//29%/P31948
- C-THYRO1001100//ZINC FINGER X-UNKEED PROTEIN ZXDA (FRAGMENT)//1.20E-67//245aa//62%/P98168
- C-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//1.30E-110//1947bp//65%/AF053700
- C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds//0//1898bp//99%/AF151835
- C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.10E-200//546aa//62%/Q05481
- 15 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence//3.80E-100//478bp//99%/AF136276
- C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT)//3.40E-51//429aa//33%/P45701
- 20 C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds//0//2330bp//94%/AF121861
- C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds//2.00E-263//3101bp//68%/AF064729
- C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (CTE-II)//1.80E-13//361aa//22%/O00154
- C-THYRO1001405//PLECTIN//6.90E-19//450aa//27%/P30427
- 25 C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-)//1.10E-131//219aa//81%/O70503
- C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B)//2.70E-171//559aa//59%/P35580
- C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT)//0//1784bp//99%/AJ002190
- 30 C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds//4.10E-273//1947bp//82%/AF175968
- C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//0//1820bp//99%/AJ225089
- 35 C-THYRO1001703//NIFR3-LIKEPROTEIN//2.90E-32//282aa//32%/P45672
- C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN)//9.30E-34//220aa//38%/Q04652
- C-THYRO1001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL)//2.40E-20//217aa//30%/P38584
- C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF)//1.40E-74//158aa//89%/P42128
- 40 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds//8.90E-205//1435bp//81%/AF171060
- C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds//0//2929bp//96%/AF126484
- C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1//2.40E-30//80aa//60%/P25916
- C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIP1) gene, complete cds//0//980bp//96%/AF180472
- 45 C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds//0//1858bp//99%/AF132936
- C-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//7.10E-71//345bp//100%/AF081192
- C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds//0//1515bp//99%/AF123534
- 50 C-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds//2.10E-50//648bp//64%/AF035207
- C-Y79AA1000313//CALPHOTIN//0.000011//336aa//23%/Q02910
- C-Y79AA1000328//SEL-10 PROTEIN//0.000000067//219aa//25%/Q93794
- C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds//0//2644bp//81%/AB030835
- C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds//0//2520bp//99%/AF081192
- C-Y79AA1000349//Mus musculus SEL-10 mRNA for RNA binding protein//0//2048bp//93%/X84691
- C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161//4.00E-20//261aa//27%/P25343
- C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete



- AMINYLTRANSFERASE) (GALNAC-T1)//1.70E-84//313aa//48%//Q07537  
 C-Y79AA1001613//ZINC FINGER PROTEIN 132//3.80E-91//209aa//41%//P52740  
 C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds//3.4e-310//1430bp//98%//AF077049  
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds//1.40E-78//  
 5 227aa//40%//Q01820  
 C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds//3.40E-  
 47//626bp//68%//AF033120  
 C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds//1.20E-258//1185bp//99%//  
 J04137  
 10 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds//  
 0//1689bp//98%//AF177145  
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds//0//2927bp//97%//  
 AF192913  
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-  
 15 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN)//4.50E-08//135aa//31%//P43489  
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7//9.40E-12//34aa//97%//P51149  
 C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds//7.10E-52//279bp//97%//  
 AF174602  
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE  
 20 SPAC10F6.02C//1.00E-10//94aa//47%//O42643  
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)//9.90E-39//143aa//52%//P42743  
 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein//5.00E-163//752bp//99%//X86018  
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.00E-257//549aa//76%//P16415  
 25 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1)//9.00E-17//120aa//45%//Q24133  
 C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L)//7.50E-09//131aa//35%//Q13329  
 C-Y79AA1002208//ANKYRIN//8.10E-34//188aa//38%//Q02357  
 C-Y79AA1002209//TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS)//1.60E-  
 72//437aa//39%//P00952  
 30 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-  
 TEIN)//0.0000018//140aa//25%//Q13829  
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3//1.70E-17//  
 146aa//35%//O16264  
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1//7.10E-17//213aa//31%//P30620  
 35 C-Y79AA1002246//SYNAPTOTAGMIN V//1.60E-28//286aa//32%//O00445  
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds//0//2106bp//99%//AB013384  
 C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds//0//1209bp//99%//AF116574  
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein//2.90E-186//1130bp//82%//  
 X67877  
 40 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit)//6.90E-140//966bp//82%//  
 Y18208  
 C-Y79AA1002399//Homo sapiens mRNA for sperm protein//0//1163bp//95%//X91879  
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds//3.9e-317//1902bp//  
 86%//U49385  
 45 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2)//9.80E-62//318aa//35%//Q04725  
 C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mR-  
 NA, complete cds//0//1545bp//96%//AF152961  
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.50E-136//472aa//  
 49%//Q05481  
 50 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//2.70E-137//340aa//  
 51%//Q05481  
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds//7.3e-311//  
 1444bp//98%//AF129534

(iii)

1. use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

- 5 2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.
- 10 3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:
- 15

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- 5     4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
6. A substantially pure protein encoded by polynucleotide of claim 4.
- 10    7. A partial peptide of the protein of claim 6.
8. An isolated polynucleotide selected from the group consisting of
- 15        (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following  
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20 (b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence  
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(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence  
 selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted,  
 inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino  
 acid sequence selected from the amino acid sequences of (b);

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the  
 nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equiv-  
 alent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein  
 encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence  
 of (a).

11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

5 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

10 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

15 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

19. A method for synthesizing a polynucleotide, the method comprising:

- 20
- a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
  - b) recovering the synthesized product.

25 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

22. A method for detecting the polynucleotide of claim 8, the method comprising:

- 30
- a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
  - b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

35 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

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Figure 1

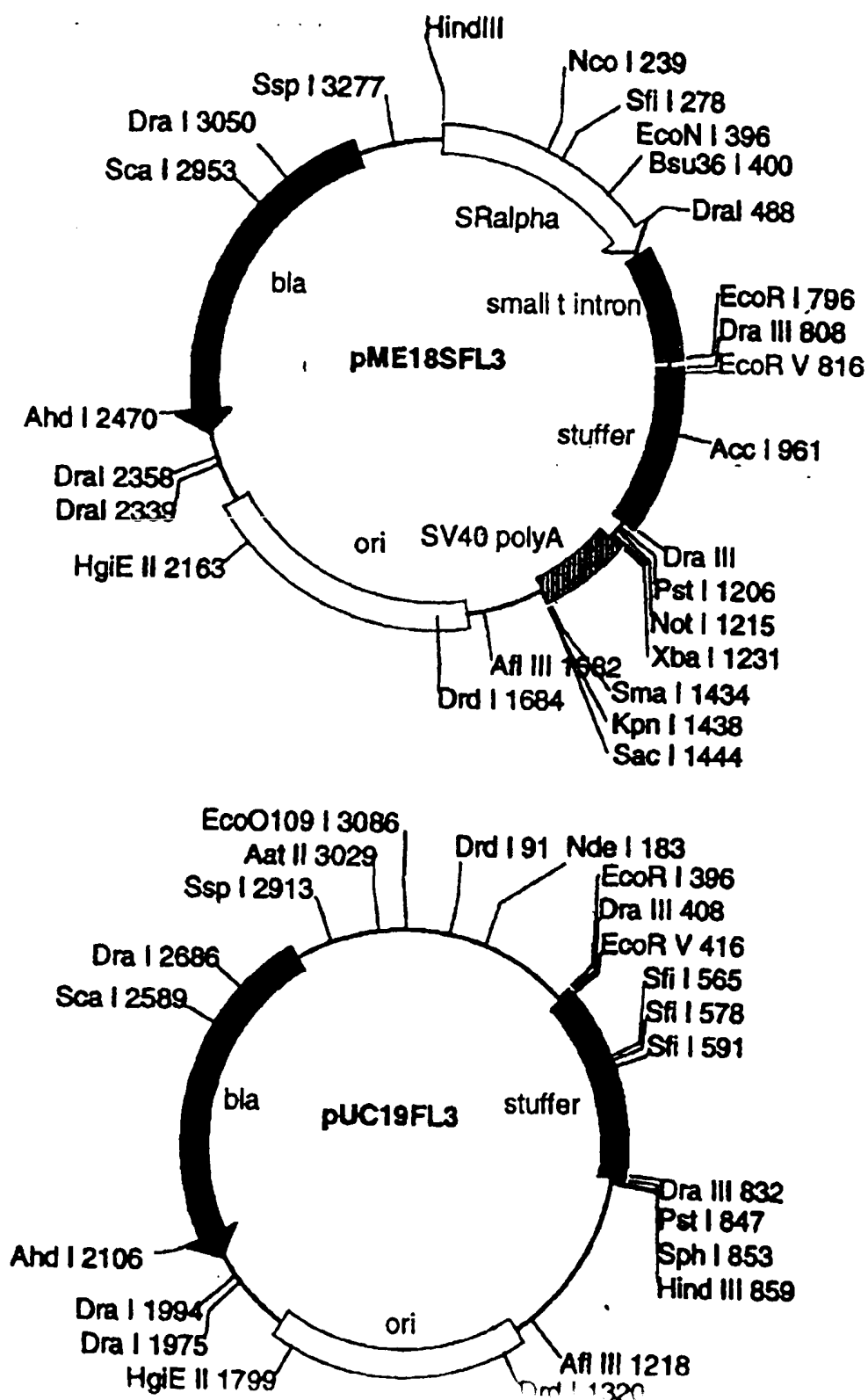


Figure 2

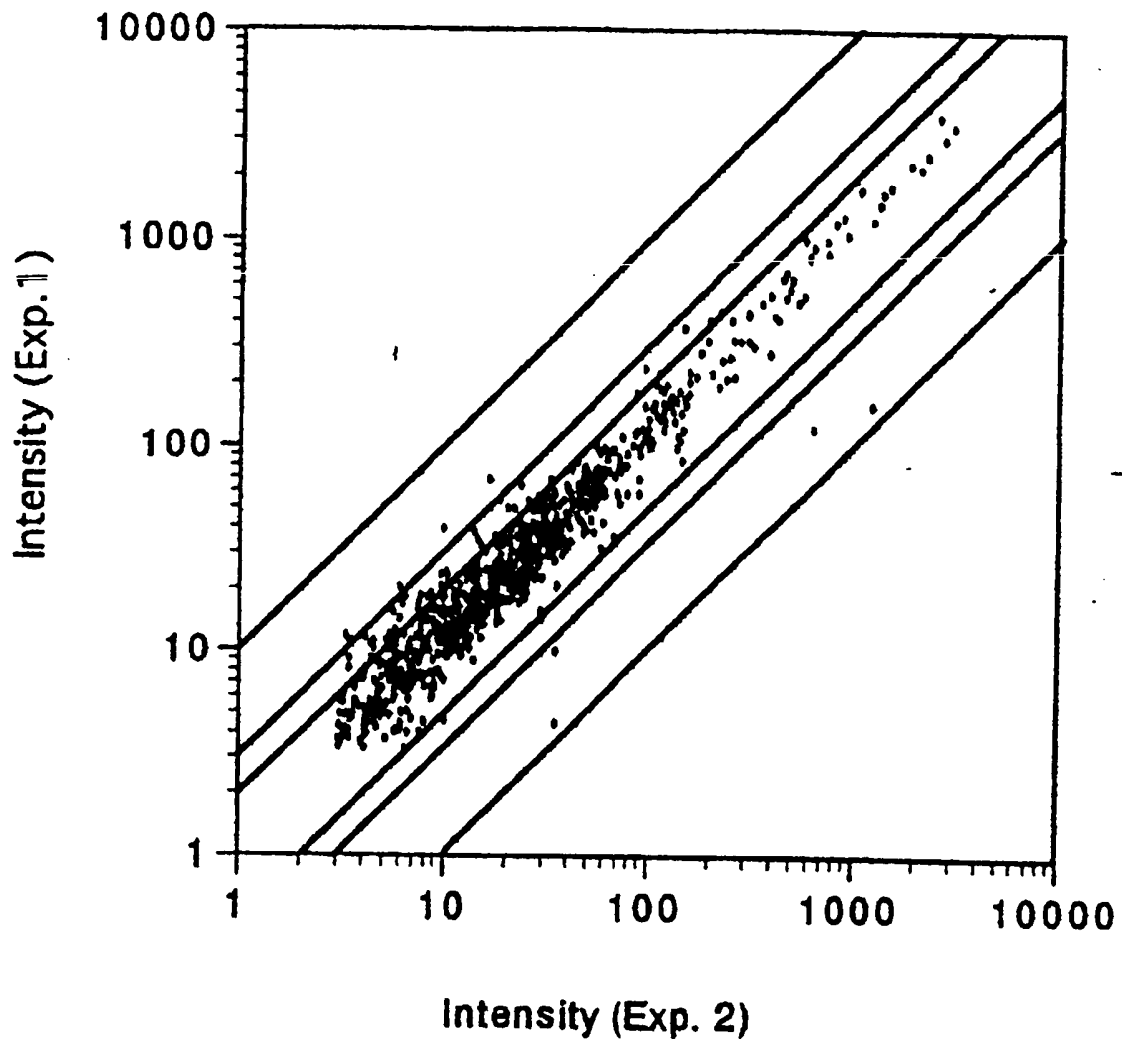


Figure 3

